

Db 95 NDRERVENAREBELTRML 111

RESULT 15

CAL2\_PARTE

ID CAL2\_PARTE STANDARD; PRT; 294 AA.

AC 094715;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE Putative cathepsin L2 (EC 3.4.22.15) (Fragment).

OS Paramacium tetraurelia.

OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;

OC Paramacium.

OX NCBI\_TaxID=5888;

RN [1]

RP SEQUENCE FROM N.A.

RC SPRAIN-Stock 51;

RX MEDLINE=96248439; PubMed=8665938;

RA Voelkel H., Kurz U., Linder J., Klumpp S., Gnan V., Jung G.,

RA Schultz J.E.;

RT "Cathepsin L is an intracellular and extracellular protease in

Paramacium tetraurelia: Purification, cloning, sequencing and specific

inhibition by its expressed propeptide.";

RL Eur. J. Biochem. 238:198-206(1996).

CC -1- FUNCTION: May be involved in extracellular digestion.

CC -1- CATALYTIC ACTIVITY: Specificity close to that of papain. As

CC compared to cathepsin B, cathepsin L exhibits higher activity

CC towards protein substrates, but has little activity on Z-Arg-Arg-

CC NMEC, and no peptidyl-dipeptidase activity.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.

CC -1- CAUTION: This protein may be non-functional as it lacks the

CC cysteine active site residue which is replaced by Gly-118.

CC -----

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CC -----

CC EMBL; X91756; CAA62871.1; -.

DR PIR; S68784; S68784.

DR HSP; O60911; 1FH0.

DR InterPro: IPR000668; Peptidase\_C1.

DR InterPro: IPR000169; SHprot\_acsite.

DR Pfam: PF00112; Peptidase\_C1; 1.

DR PRINTS; PR00705; PAPA1N.

DR PRODOM; PD000158; Peptidase\_C1; 1.

DR SMART; SM00645; Pept\_C1; 1.

DR PROSITE; PS00640; THIOL\_PROTEASE ASN; FALSE\_NEG.

DR PROSITE; PS00139; THIOL\_PROTEASE CYS; FALSE\_NEG.

DR PROSITE; PS00639; THIOL\_PROTEASE\_HIS; FALSE\_NEG.

DR HydroLase; Thiol protease.

KW HydroLase; Thiol protease.

FT NON\_TER 1

FT PROPEP 1

FT CHAIN 1

FT SITE 118 118

FT ACT\_SITE 247 247

FT ACT\_SITE 264 264

FT DISULFID 115 156

FT DISULFID 240 284

SQ SEQUENCE 294 AA; 33627 MW; 6FD686A0176BEC51 CRC64;

Query Match 45.88; Score 38; DB 1; Length 294;

Best Local Similarity 66.7%; Pred. No. 29;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 SNKTRIDEANOR 12

DB 40 SNKRMIEENOR 51

Search completed: September 16, 2003, 19:27:08  
Job time : 4.42857 secs

RA Sharypova L.A., Yurgel S.N., Keller M., Simarov B.V., Puehler A.,  
 RA Becker A.;  
 RT "The eff-482 locus of Sinorhizobium meliloti CXM1-105 that influences  
 RT symbiotic effectiveness consists of three genes encoding an  
 RT endoglycanase, a transcriptional regulator and an adenylate cyclase.";   
 RL Mol. Genet. 261:1032-1044(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1021;  
 RX MEDLINE=21396509; PubMed=11481432;  
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,  
 RA Barloy-Hubier F., Bowser L., Cabela D., Gallbert F., Gouzy J.,  
 RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,  
 RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,  
 RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;  
 RT "Nucleotide sequence and predicted functions of the entire  
 RT Sinorhizobium meliloti pSym megaplasmid";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).  
 CC -1- FUNCTION: SEEMS TO AFFECT THE TRANSCRIPTION OF CVA3. MAY BE  
 CC NEGATIVELY AUTOREGULATED.  
 CC -1- SIMILARITY: BELONGS TO THE SYRB FAMILY.  
 CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO TWO  
 CC FRAMESHIFTS IN POSITION 124 AND 137.  
 CC -----  
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 CC -----  
 DR EMBL; AJ225896; CAB8102.1; ALT\_FRAME.  
 DR EMBL; AE007273; AAK65521.1; -.  
 DR PIR; G95369; G95369.  
 DR InterPro: IPR002514; Transposase\_8.  
 DR Pfam: PF01527; Transposase\_8; 1.  
 DR Nomenclature: Transcription regulation; Repressor; Plasmid;  
 KW Complete proteome.  
 FT CONFLICT 17 17 N -> H (IN REF. 1).  
 SO SEQUENCE 151 AA; 17028 MW; 215627A0FAD4EBA8 CRC64;  
 QY  
 Db 5 RIDEANORATKML 17  
 121 RLEENORUKL 133  
 RESULT 14  
 ARF2\_MOUSE  
 ID ARF2\_MOUSE STANDARD: PRT; 181 AA.  
 AC P16500; P10947;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE ADP-ribosylation factor 2.  
 GN ARF2.  
 OS Mus musculus (Mouse).  
 OS Rattus norvegicus (Rat), and  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090, 10116, 9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Bovine;  
 RX MEDLINE=88289746; PubMed=3135549;  
 RA Price S.R., Nightingale M., Tsai S.-C., Williamson K.C., Adamik R.,  
 RA Chen H.-C., Moss J., Vaughan M.;  
 RT "Guanine nucleotide-binding proteins that enhance cholesterol ADP-

RT ribosyltransferase activity: nucleotide and deduced amino acid  
 RT sequence of an ADP-ribosylation factor cDNA.";   
 RL Proc. Natl. Acad. Sci. U.S.A. 85:5488-5491(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Bovine; TISSUE=Retina;  
 RX MEDLINE=93186792; PubMed=8444865;  
 RA Servent I.M., Cavanaugh E., Moss J., Vaughan M.;  
 RT "Characterization of the gene for ADP-ribosylation factor (ARF) 2, a  
 RT developmentally regulated, selectively expressed member of the ARF  
 RT family of approximately 20-kDa guanine nucleotide-binding proteins.";   
 RL J. Biol. Chem. 268:4863-4872(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Rat; TISSUE=Brain;  
 RA Nightingale M.S., Price S.R., Tsuchiya M., Moss J., Vaughan M.;  
 RN Submitted (XXX-1994) to the EMBL/Genbank/DBD databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Mouse; STRAIN=ICR; TISSUE=Brain;  
 RX MEDLINE=97103475; PubMed=8947846;  
 RA Hosaka M., Toda K., Takatsu H., Torii S., Murakami K., Nakayama K.;  
 RT "Structure and intracellular localization of mouse ADP-ribosylation  
 RT factors type 1 to type 6 (ARF1-ARF6).";   
 RL J. Biochem. 120:813-819(1996).  
 CC -1- FUNCTION: GTP-BINDING PROTEIN THAT FUNCTIONS AS AN ALLOSTERIC  
 CC ACTIVATOR OF THE CHOLERA TOXIN CATALYTIC SUBUNIT, AN ADP-  
 CC RIBOSYLTRANSFERASE. INVOLVED IN PROTEIN TRAFFICKING; MAY MODULATE  
 CC VESICLE BUDDING AND UNCOATING WITHIN THE GOLGI APPARATUS.  
 CC -1- SIMILARITY: BELONGS TO THE ARF FAMILY OF GTP-BINDING PROTEINS.  
 CC -----  
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 CC -----  
 DR EMBL; J03794; AAA30383.1; -.  
 DR EMBL; M88287; AAA30754.1; -.  
 DR EMBL; M88282; AAA18982.1; -.  
 DR EMBL; M88289; AAA18982.1; JOINED.  
 DR EMBL; M88290; AAA18982.1; JOINED.  
 DR EMBL; M88291; AAA18982.1; JOINED.  
 DR EMBL; L12381; AAA40686.1; -.  
 DR EMBL; D87899; BAA13491.1; -.  
 DR PIR; A45422; A45422.  
 DR PIR; JC4946; JC4946.  
 DR HSP; P32889; 1HUR.  
 DR MGD; MG1:99595; Arf2.  
 DR InterPro: IPR006688; ARF.  
 DR InterPro: IPR006689; ARF/SAR.  
 DR InterPro: IPR001806; Ras\_transfmr.  
 DR InterPro: IPR005225; Small\_GTP.  
 DR Pfam: PF00025; arf; 1.  
 DR PRINTS: PRO0449; RASTRNSFRMNG.  
 DR PRINTS: PRO0328; SARIGTBP.  
 DR SMART; SM00177; ARF; 1.  
 DR TIGRFAMS; TIGR00231; small\_GTP; 1.  
 DR PROSITE; PS01019; ARF; 1.  
 KW GTP-binding; Multigene family; Protein transport; Golgi stack.  
 FT NP\_BIND 24 31 GTP (BY SIMILARITY).  
 FT NP\_BIND 67 71 GTP (BY SIMILARITY).  
 FT NP\_BIND 126 129 GTP (BY SIMILARITY).  
 SO SEQUENCE 181 AA; 20746 MW; 95BE17A962B83016 CRC64;  
 QY  
 Query Match 45.8%; Score 38; DB 1; Length 181;  
 Best Local Similarity 35.3%; Pred. No. 17;  
 Matches 6; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
 1 SNKTRIDEANORATKML 17  
 :::::|:::|:::|

RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,  
 RA Emanuel B.S., Shaikh T., Kuranashi H., Saitta S., Budarf M.L.,  
 RA McDermid H.E., Johnson A., Wong A.C., Morrow B.E., Edelmann L.,  
 RA Kim U.J., Shizuya H., Simon M.I., Dunanski J.P., Peyraud M., Kedra D.,  
 RA Seroussi E., Fransson I., Tapia I., Bruders C.E., O'Brien K.P.,  
 RA Wilkinson P., Bodenreich A., Hartman K., Hu X., Khan A.S., Lane L.,  
 RA Tiliun Y., Wright H.,  
 RT "The DNA sequence of human chromosome 22.";  
 RL Nature 402:489-495(1999).

RN [3]  
 RN SEQUENCE FROM N.A.

RC TISSUE=Brain;  
 RX MEDLINE=2238257; PubMed=12477932;

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullane C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Prillay S.J.,  
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettleman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield V.S.N., Krzywinski M.I., Skalski U., Smallus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [4]  
 RN SEQUENCE OF 650-970 FROM N.A.

RC TISSUE=Testis;  
 RX OTTENWELDER B., OBERMATER B., MEWES H.-W., GASENHUBER J.,  
 RA WILMANN S.;

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in smooth muscle, pancreas  
 CC and testis.

CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous  
 CC gene model prediction.

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CC EMBL: AB020659; BAA74875.1;  
 DR EMBL: AC004542; AAC12954.1; ALT\_SEQ.  
 DR EMBL: BC019257; AAH19257.1;  
 DR EMBL: AL133637; CAB63760.1;  
 DR PIR: T43455; T43455.

KW Coiled coil.  
 FT DOMAIN 220 300 COILED COIL (POTENTIAL).  
 FT DOMAIN 485 522 COILED COIL (POTENTIAL).  
 FT DOMAIN 679 699 COILED COIL (POTENTIAL).  
 FT DOMAIN 904 954 COILED COIL (POTENTIAL).  
 FT SEQUENCE 970 AA: 110724 MW: 459161807BB85366 CRC64;

Query Match 47.0%; Score 39; DB 1; Length 970;  
 Best Local Similarity 69.2%; Pred. No. 71;

Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 KTRIDEANORATK 15  
 DB 287 KRIKEAKORALK 299

RESULT 12  
 YAMB\_CAEEL STANDARD; PRT; 918 AA.  
 ID YAMB\_CAEEL  
 AC P34487;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical protein F59B2.12 in chromosome III.  
 DE F59B2.12.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Pelodertinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RN SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,  
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,  
 RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,  
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,  
 RA Sims M., Smaildon N., Smith A., Smith M., Sonnenhammer E., Staden K.,  
 RA Sulston J., Thierry-Mieg Y., Thomas K., Vaudin M., Vaughan K.,  
 RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,  
 RA Woldman P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans.";  
 RL Nature 368:32-38(1994).

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CC EMBL: 211505; CAA7581.1;  
 DR PIR: G88545; G88545.  
 DR WormPep: F59B2.12; CE01024.

KW Hypothetical protein.  
 KW SEQUENCE 918 AA: 96560 MW: E464PD86B14945DE CRC64;

Query Match 46.4%; Score 38.5; DB 1; Length 918;  
 Best Local Similarity 62.5%; Pred. No. 82;  
 Matches 10; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

OY 1 SNKT---RIDEANORA 13  
 DB 368 SNKTDNALDEANOSA 383

RESULT 13  
 SYB2\_RHIME STANDARD; PRT; 151 AA.

ID SYB2\_RHIME  
 AC 092301;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Probable transcriptional regulator syb2.  
 DE GN syb2 OR RA0863 OR SMA1586.  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OS Plasmid pSyma (megaplasmid 1).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.  
 OX NCBI\_TaxID=382;  
 RN [1]  
 RN SEQUENCE FROM N.A.

RC STRAIN=CM1-105;  
 RX MEDLINE=99413305; PubMed=10485295;

FT	REPAT	226	293	BIR 2..
PT	ZN_FING	391	426	RING-TYPE.
SEQ	SEQUENCE	438 AA:	48098 MW:	ACC2JC08EDF5AEF29 CRC64:
Query Match		47.0%:	Score 39:	DB 1; Length 438;
Best Local Similarity		40.0%:	Pred. No. 30:	
Matches	6;	Conservative	6;	Mismatches 3; Indels 0; Gaps 0;
OY	2 NKTIDEANQRA	16		
DB	34 NKTMRNDLNRETR	48		
RESULT 11				
K852_HUMAN	STANDARD;	PRT;	970 AA.	
ID	K852_HUMAN			
AC	O9Y6X9; O9UF28; O9YCV2;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Protein KIAA0852.			
GN	KIAA0852.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=99156230; PubMed=10048485;			
RA	Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosewa M.,			
RA	Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;			
RT	"Prediction of the coding sequences of unidentified human genes. XII.			
RT	The complete sequences of 100 new cDNA clones from brain which code			
RT	for large proteins in vitro."			
RL	DNA Res. 5:355-364(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20057165; PubMed=10591208;			
RA	Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,			
RA	Clamp M., Smith L.J., Ainscough R., Almeida J.P., Babbage A.K.,			
RA	Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,			
RA	Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,			
RA	Burhill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,			
RA	Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,			
RA	Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,			
RA	Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,			
RA	Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,			
RA	Gilbert J.G.R., Goward M.E., Graham D.V., Griffiths M.N.D., Hall C.,			
RA	Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,			
RA	Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,			
RA	Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,			
RA	Matyn I.D., Mashrogh-Mohammadi M., Matthews L.H., Mccann O.T.,			
RA	Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,			
RA	Odel C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,			
RA	Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,			
RA	Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,			
RA	Soderlund C., Spragon L., Steward C.A., Sultson J.E., Swann R.M.,			
RA	Vandin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,			
RA	Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,			
RA	Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shmizu N.,			
RA	Mitoshiba S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,			
RA	Shutani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuayama S.,			
RA	Roe B.A., Chen F., Chu Y., Crabtree J., Deschamps S., Do A., Do T.,			
RA	Dorman A., Pang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.T.,			
RA	Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,			
RA	Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,			
RA	Wang Q., Wang Y., Wang Z., White J., Williamson D., Wu H., Yao Z.,			
RA	Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,			
RA	Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,			
RA	Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins T.,			
RA	Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfs T.,			
RA	Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,			

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RA Saint-Onge A., Romeyer F., Lebel P., Masson L., Brousseau R.;
RT "Specificity of the pseudomonas aeruginosa PAOI lipoprotein I gene as
RL a DNA probe and PCR target region within the Pseudomonadaceae.";
RN J. Gen. Microbiol. 138:733-741(1992).
RP
RC SEQUENCE FROM N.A.
RX STRAIN-ATCC 15692 / PAOI;
RA MEDLINE-20437337; PubMed-10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Laird K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.R.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Salter M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -I- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
CC anchor.
CC
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CC
CC EMBL: X13748; CAA32013.1; -
DR EMBL: M25761; AA25880.1; -
DR EMBL: X58714; CAA41350.1; -
DR EMBL: A07695; CAA00707.1; -
DR EMBL: AE004712; AAG06241.1; -
DR PIR: A33854; A33854.
DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
KW Outer membrane; Lipoprotein; Signal; Complete proteome.
FT SIGNAL 1 19
FT CHAIN 20 83 MAJOR OUTER MEMBRANE LIPOPROTEIN.
FT LIPID 20 20 N-ACYL DIGLYCERIDE.
SQ SEQUENCE 83 AA; 8835 MW; E87F52B86B04DBA4 CRC64;

Query Match 50.6%; Score 42; DB 1; Length 83;
Best Local Similarity 72.7%; Pred. No. 1.4;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 DEANORATKML 17
DB 67 DEANERALLML 77

RESULT 8
YE09 YEAST STANDARD; PRT; 420 AA.
AC P40038;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical 47.0 kDa protein in PET117-CEM1 intergenic region.
GN YER059M.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RX PubMed-9169868;
RA Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
RA Ararajo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
RA Cherry J.M., Chung E., Duncan M., Guzman T., Hartzell G.,
RA Hunnicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
RA Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oeffner P.,
RA Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,

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RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
RL Nature 387:78-81(1997).
CC -I- SIMILARITY: TO YEAST YII050M.
CC
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CC
CC EMBL: U1813; AAB64595.1; -
DR PIR: S50562; S50562.
DR SGD: S0000861; PCL6.
DR GO: GO:0005979; P:regulation of glycogen biosynthesis; IGI.
DR GO: GO:0005981; P:regulation of glycogen catabolism; IGI.
KW Hypothetical protein.
SQ SEQUENCE 420 AA; 47007 MW; BD8A0C7A501C94E5 CRC64;

Query Match 50.0%; Score 42; DB 1; Length 420;
Best Local Similarity 50.0%; Pred. No. 8.5;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 1 SNKTRIDEANORATKM 16
DB 283 SNESSLDKANRGADKM 298

RESULT 9
PR11 YEAST STANDARD; PRT; 494 AA.
AC P49704;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE pre-mRNA splicing factor PRP31.
GN PRP31 OR YGR091M.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE-96184869; PubMed-8604353;
RA Weidenhammer E.M., Singh M., Ruiz-Noriega M., Woolford J.L., Jr.;
RT "The PRP31 gene encodes a novel protein required for pre-mRNA
RT splicing in Saccharomyces cerevisiae.";
RL Nucleic Acids Res. 24:1164-1170(1996).
RN
RP SEQUENCE FROM N.A.
RA Medler H., Scharfe M., Medler E., Wambutt R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -I- SUBCELLULAR LOCATION: Nuclear (Potential).
CC
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CC or send an email to license@sdb-sib.ch).
CC
CC EMBL: U31970; AAB74984.1; -
DR PIR: S54386; S54386.
DR SGD: S0003123; PRP31.
DR GO: GO:0030532; C:small nuclear ribonucleoprotein complex; IDA.
DR GO: GO:0008248; F:pre-mRNA splicing factor activity; IPI.
DR GO: GO:0006371; P:mRNA splicing; IPI.
DR InterPro: IPR002687; Nop.

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RESULT 6	SN25_DROME	STANDARD:	PRT:	212 AA.
ID	SN25_DROME			
AC	P36975.			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Synaptoosomal-associated protein 25 (SNAP-25).			
GN	SNAP25.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
XX	NCBI_Taxid=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TTISSUE=Head:			
RA	MEDLINE=94043281; PubMed=8226991;			
RA	Risinger C., Blomqvist A.G., Lundell I., Lambertsson A.,			
RA	Nassel D., Pieribone V.A., Brodin L., Larhammar D.;			
RT	"Evolutionary conservation of synaptoosome-associated protein 25 kDa			
RT	(SNAP-25) shown by Drosophila and Torpedo cDNA clones.";			
J. Biol. Chem.	268:24408-24414(1993).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=97417485; PubMed=9272858;			
RA	Risinger C., Delcher D.L., Lundell I., Schwarz T.L., Larhammar D.;			
RT	"Complex gene organization of synaptic protein SNAP-25 in Drosophila			
RT	melanogaster.";			
Gene	194:169-177(1997).			
CC	-1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE SYNAPTIC FUNCTION OF			
CC	SPECIFIC NEURONAL SYSTEMS ASSOCIATED WITH PROTEINS INVOLVED IN			
CC	VESICLE DOCKING AND MEMBRANE FUSION.			
CC	-1- SUBCELLULAR LOCATION: COMPLEXED WITH MACROMOLECULAR ELEMENTS OF			
CC	THE NERVE TERMINAL.			
CC	-1- TISSUE SPECIFICITY: EXCLUSIVELY FOUND IN BRAIN AND GANGLIA.			
CC	-1- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.			
CC	-1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.			
CC	-----			
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Query Match	54.28;	Score 45;	DB 1;	Length 212;
Best Local Similarity	58.8%;	Pred. No. 1.2;		
Matches 10;	Conservative 3;	Mismatches 4;	Indels 0;	Gaps 0;

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Oy      1  SNKTRIDEANORATKML 17
        ||: || ||||| :||
Db      195  SNEARIIVANORAHOLL 211

RESULT 7
MULTI_PSEAE
ID      MULTI_PSEAE      STANDARD;      PRT;      83 AA.
AC      P11221;
DT      01-JUL-1989 (Rel. 11, Created)
DT      01-JUL-1989 (Rel. 11, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Major outer membrane lipoprotein precursor (Murein-lipoprotein)
        (lipoprotein I).
GN      OPRI OR PA2853.
OS      Pseudomonas aeruginosa.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OX      Pseudomonadaceae; Pseudomonas.
        NCHI_TaxID=287;
        [1]
RN      SEQUENCE FROM N.A.
RC      STRAIN=Isolate PA2;
RX      MEDLINE=69313294; PubMed=2473376;
RA      Cornelis P., Bouia A., Belarbi A., Guyonvarch A., Kammerer B.,
RT      Hannart V., Hubert J.-C.;
        "Cloning and analysis of the gene for the major outer membrane
        lipoprotein from Pseudomonas aeruginosa.";
        Mol. Microbiol. 3:421-428(1989).
        [2]
RN      SEQUENCE FROM N.A.
RX      MEDLINE=89327122; PubMed=2502533;
RA      Duchene M., Barron C., Schweizer A., von Sprecht B.-U., Domdey H.;
RT      "Pseudomonas aeruginosa outer membrane lipoprotein I gene: molecular
        cloning, sequence, and expression in Escherichia coli.";
        J. Bacteriol. 171:4130-4137(1989).
        [3]
RN      SEQUENCE FROM N.A.
RC      STRAIN=ATCC 15692 / PA01;
RX      MEDLINE=92268853; PubMed=1586307;

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OC Torpediniformes; Torpedinoidae; Torpedinidae; Torpedo.
ON NCB1_TaxID=7788;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Electric lobe;
RX MEDLINE=94043281; PubMed=8226991;
RA Räsinger C., Blomqvist A.G., Lundell I., Lambertson A.,
RA Nassel D., Pieribone V.A., Brodin L., Larhammar D.;
RT "Evolutionary conservation of synaptosome-associated protein 25 kDa
RT (SNAP-25) shown by Drosophila and Torpedo cDNA clones.";
RL J. Biol. Chem. 268:24408-24414(1993).
CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE SYNAPTIC FUNCTION OF
CC SPECIFIC NEURONAL SYSTEMS. ASSOCIATES WITH PROTEINS INVOLVED IN
CC VESICLE DOCKING AND MEMBRANE FUSION.
CC -1- SUBCELLULAR LOCATION: COMPLEXED WITH MACROMOLECULAR ELEMENTS OF
CC THE NERVE TERMINAL.
CC -1- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.
CC -1- SIMILARITY: CONTAINS 2 t-SNARE COILED-COIL HOMOLOGY DOMAINS.
CC -----
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CC -----
DR EMBL: I22020; AAA49284.1; -
DR PIR: I50552; I50552.
DR InterPro: IPR000928; SNAP-25.
DR InterPro: IPR000727; t-SNARE.
DR Pfam: PF00835; SNAP-25; 1.
DR SMART: SM00397; t-SNARE; 2.
DR PROSITE: PS00192; t-SNARE; 2.
KM Synaptosome: Neutrone: Repeat: Coiled coil.
FT DOMAIN 23 85 t-SNARE COILED-COIL HOMOLOGY 1.
FT DOMAIN 147 209 t-SNARE COILED-COIL HOMOLOGY 2.
FT DOMAIN 88 96 CYS-RICH.
SQ SEQUENCE 210 AA; 23652 MW; 58FE471A92348B81 CRC64;

Query Match 78.3%; Score 65; DB 1; Length 210;
Best Local Similarity 81.2%; Pred. No. 0.0004;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NKTRIDEANORATKML 17
DB 195 NKARIDEANKHATKML 210

RESULT 5
SN23_HUMAN
ID SN23_HUMAN STANDARD; PRT; 211 AA.
AC 000161; 000162; 013602;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Synptosome1-associated protein 23 (SNAP-23) (Vesicle-membrane fusion
DE protein SNAP-23).
GN SNAP23.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-23A).
RC TISSUE-B-cell;
RX MEDLINE=96278745; PubMed=8663154;
RA Ravichandran V., Chawla A., Roche P.A.;
RT "Identification of a novel syntaxin- and synaptobrevin/VAMP-binding
RT protein, SNAP-23, expressed in non-neuronal tissues.";
RL J. Biol. Chem. 271:13300-13303(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS SNAP-23A AND SNAP-23B).
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RC TISSUE-Neutrophils;
RX MEDLINE=97224437; PubMed=9070898;
RA Molinero F., Lazo P.A.;
RT "Identification of two isoforms of the vesicle-membrane fusion protein
RT SNAP-23 in human neutrophils and HL-60 cells.";
RL Biochem. Biophys. Res. Commun. 231:808-812(1997).
RN [3]
RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RA Nadal M., Area E., Molinero F., Estyvil X., Lazo P.A.;
RT "Exon organization and chromosomal localization of human synptosomal
RT associated protein-23 (SNAP-23) gene and generation of isoforms by
RT alternative splicing.";
RL Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-23A).
RC TISSUE-Cervix, Placenta, and Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Woley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: ESSENTIAL COMPONENT OF THE HIGH AFFINITY RECEPTOR FOR
CC OF TRANSPORT VESICLE DOCKING AND FUSION.
CC -1- SUBUNIT: BINDS TIGHTLY TO MULTIPLE SYNTAXINS AND
CC SYNAPTOBREVINS/VAMPS.
CC -1- SUBCELLULAR LOCATION: MAINLY LOCALIZED TO THE PLASMA MEMBRANE.
CC -1- ALTERNATIVE PRODUCTS:
CC Name=SNAP-23a;
CC IsoId=000161-1; Sequence=Displayed;
CC Name=SNAP-23b;
CC IsoId=000161-2; Sequence=VSP_006187, VSP_006188;
CC -1- TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST LEVELS WHERE FOUND IN
CC PLACENTA.
CC -1- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.
CC -1- SIMILARITY: CONTAINS 2 t-SNARE COILED-COIL HOMOLOGY DOMAINS.
CC -----
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CC -----
DR EMBL: U55936; AAC50537.1; -
DR EMBL: Y09567; CAAT0760.1; -
DR EMBL: Y09568; CAAT0761.1; -
DR EMBL: A011915; CAA09864.1; -
DR EMBL: BC000148; AAH00148.1; -
DR EMBL: BC003686; AAH003686.1; -
DR EMBL: BC022890; AAH22890.1; -
DR PIR: JCS296; JCS296.
DR PIR: JCS297; JCS297.
DR Genew; HGNC:11131; SNAP23.
DR MIM; 602534; -.
```

RA Jensen M.J., Smith L.A.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Mouse; STRAIN=BALB/C;  
 RX MEDLINE=90078337; PubMed=2592413;  
 RA Oyler G.A., Hignins G.A., Hart R.A., Battenberg E., Billingsley M.,  
 Bloom F.E., Wilson M.C.;  
 RT "The identification of a novel synaptosomal-associated protein,  
 SNAP-25, differentially expressed by neuronal subpopulations";  
 RL J. Cell Biol. 109:3039-3052(1989).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Mouse; STRAIN=C57BL/6; TISSUE=Eye;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Schein C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong F.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Vallatton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 Scherter J.E., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [8]  
 RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).  
 RC SPECIES=Cat;  
 RX Katoaka M.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Cat; TISSUE=Brain;  
 RX Cho A.R., You K.H.;  
 RT "Cloning of the SNAP-25 gene from a rat brain cDNA library";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [10]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Chicken; TISSUE=Retina;  
 RX MEDLINE=91126080; PubMed=1992470;  
 RA Catsicas S., Lachmanar D., Blomqvist A., Sanna P.P., Milner R.J.,  
 Wilson M.C.;  
 RT "Expression of a conserved cell-type-specific protein in nerve  
 terminals coincides with synaptogenesis";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:785-789(1991).  
 RN [11]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC SPECIES=Chicken;  
 RX MEDLINE=93389738; PubMed=8377193;  
 RA Bark I.C.;  
 RT "Structure of the chicken gene for SNAP-25 reveals duplicated exon  
 encoding distinct isoforms of the protein";  
 RL J. Mol. Biol. 233:67-76(1993).  
 RN [12]  
 RP PALMITOYLATION.  
 RC SPECIES=Cat;  
 RX MEDLINE=93100552; PubMed=1281490;  
 RA Hess D.T., Slater T.M., Wilson M.C., Skene J.H.P.;  
 RT "The 25 kDa synaptosomal-associated protein SNAP-25 is the major  
 methionine-rich polypeptide in rapid axonal transport and a major  
 substrate for palmitoylation in adult CNS";  
 RL J. Neurosci. 12:4634-4641(1992).  
 RN [13]

RP SUBCELLULAR LOCATION OF RNA TRANSCRIPTS.  
 RC SPECIES=Cat;  
 RX MEDLINE=96346613; PubMed=8738135;  
 RA Jacobsson G., Plehl F., Bark I.C., Zhang X., Meister B.;  
 RT "Differential subcellular localization of SNAP-25a and SNAP-25b RNA  
 transcripts in spinal motoneurons and plasticity in expression after  
 nerve injury";  
 RL Brain Res. Mol. Brain Res. 37:49-62(1996).  
 CC - FUNCTION: tSNARE involved in the molecular regulation of  
 neurotransmitter release. May play an important role in the  
 synaptic function of specific neuronal systems. Associates with  
 proteins involved in vesicle docking and membrane fusion.  
 CC - SUBUNIT: Binds to syntaxin-1.  
 CC - ALTERNATIVE PRODUCTS:  
 Event-Alternative splicing: Named isoforms=2;  
 Comment=Isoforms differ by the usage of two alternative  
 homologous exons (5a and 5b) which encode for positions 56 to 94  
 and differ only in 9 positions out of 39;  
 Name=SNAP-25b;  
 IsoId=P13795-1; Sequence=Displayed;  
 Name=SNAP-25a;  
 IsoId=P13795-2; Sequence=VSP\_006186;  
 Note=Has been shown to exist only in human and rat so far;  
 CC - TISSUE SPECIFICITY: NEURONS OF THE NEOCORTEX, HIPPOCAMPUS,  
 PIRIFORM CORTEX, ANTERIOR THALAMIC NUCLEI, PONTINE NUCLEI, AND  
 GRANULE CELLS OF THE CEREBELLUM.  
 CC - PM: PALMITOYLATED.  
 CC - SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.  
 CC - SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.  
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 CC -----  
 DR EMBL: L19761; AAC37546.1; -  
 DR EMBL: L19760; AAC37545.1; -  
 DR EMBL: D21267; BAA22370.1; -  
 DR EMBL: AL023913; CAB42860.1; -  
 DR EMBL: AL023913; CAC34534.1; -  
 DR EMBL: AF240770; AAF64477.1; -  
 DR EMBL: M22012; AAA61741.1; -  
 DR EMBL: BC018249; AAH18249.1; -  
 DR EMBL: M57957; AAA49072.1; -  
 DR EMBL: AF245227; AAF81202.1; -  
 DR EMBL: AB003991; BAA20151.1; -  
 DR EMBL: AB003992; BAA20152.1; -  
 DR EMBL: L09253; AAA49070.1; -  
 DR EMBL: L09254; AAA49070.1; JOINED.  
 Query Match 100.0%; Score 83; DB 1; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SNKTRIDEANORATKML 17  
 DB 187 SNKTRIDEANORATKML 203  
 ID SN25\_TORMA STANDARD; PRT; 210 AA.  
 AC P36976;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Synaptosomal-associated protein 25 (SNAP-25).  
 OS Torpedo marmorata (Marbled electric ray).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Squalae; Hypnosqualeae; Pristiogaster; Batoidae;



Query Match 100.0%; Score 83; DB 1; Length 203;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SNKTRIDEANORATKML 17  
 DB 184 SNKTRIDEANORATKML 200

RESULT 2  
 SN2L\_CARAU STANDARD; PRT; 204 AA.  
 ID SN2L\_CARAU  
 AC P36977;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Synaptosomal-associated protein 25a (SNAP-25a).  
 GN SNAP-A.  
 OS Carassius auratus (Goldfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Carassius.  
 OC NCBI\_TaxID=957;  
 RX MEDLINE=94068448; PubMed=8248151;  
 RA Ristinger C., Larhammer D.;  
 RT "Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish."  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).  
 CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE SYNAPTIC FUNCTION OF SPECIFIC NEURONAL SYSTEMS. ASSOCIATES WITH PROTEINS INVOLVED IN VESICLE DOCKING AND MEMBRANE FUSION.  
 CC -1- SUBCELLULAR LOCATION: COMPLEXED WITH MACROMOLECULAR ELEMENTS OF THE NERVE TERMINAL.  
 CC -1- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.  
 CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL: L22973; AAA16537.1; -  
 DR PIR: I50480; I50480.  
 DR InterPro: IPR000928; SNAP-25.  
 DR Pfam: PFO0835; SNAP-25; 1.  
 DR SMART: SM00397; t-SNARE; 2.  
 DR PROSITE: PS50192; T-SNARE; 2.  
 KW Synaptosome; Neuron; Repeat; Coiled coil; Multigene family.  
 FT DOMAIN 19 81 T-SNARE COILED-COIL HOMOMOLOGY 1.  
 FT DOMAIN 138 200 T-SNARE COILED-COIL HOMOMOLOGY 2.  
 FT DOMAIN 85 92 CYS-RICH.  
 SQ SEQUENCE 204 AA; 22843 MW; 458BBEFCFC09189 CRC64;

Query Match 100.0%; Score 83; DB 1; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SNKTRIDEANORATKML 17  
 DB 185 SNKTRIDEANORATKML 201

RESULT 3  
 SN25\_HUMAN STANDARD; PRT; 206 AA.  
 ID SN25\_HUMAN  
 AC P13795; P36974;

DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Synaptosomal-associated protein 25 (SNAP-25) (Super protein) (SUP).  
 GN SNAP25 OR SNAP.  
 OS Homo sapiens (Human).  
 OS Macaca mulatta (Rhesus macaque).  
 OS Mus musculus (Mouse).  
 OS Rattus norvegicus (Rat).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606, 9544, 10090, 10116, 9031;  
 RX MEDLINE=94156217; PubMed=8112622;  
 RA Bark I., Wilson M.C.;  
 RT "Human cDNA clones encoding two different isoforms of the nerve terminal protein SNAP-25."  
 RL Gene 139:291-292(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Human; TISSUE=Brain;  
 RX MEDLINE=94333829; PubMed=8056350;  
 RA Zhao N., Hashida H., Takahashi N., Sakaki Y.;  
 RT "Cloning and sequence analysis of the human SNAP25 cDNA."  
 RL Gene 145:313-314(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC SPECIES=Human; TISSUE=Skeletal muscle;  
 RX MEDLINE=96332494; PubMed=8760387;  
 RA Jagadeish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L.,  
 RA Gough K.H., Grusovin J., Verkuylen A., Cosgrove L., Alafael A.,  
 RA Frenkel M.J., Ward C.W.;  
 RT "Insulin-responsive tissues contain the core complex protein SNAP-25 (synaptosomal-associated protein 25) A and B isoforms in addition to syntaxin 4 and synaptobrevins 1 and 2."  
 RL Biochem. J. 317:945-954(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Human;  
 RX MEDLINE=21638749; PubMed=11780052;  
 RA Deloulkas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deaman R., Dhani P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Leveasialho M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConachie L.J., McLean K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Paiker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
 RA Stuce C.D., Smith M.L., Soderlund C., Steward C.A., Sultson J.E.,  
 RA Swan R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin R., Walli M., Wallis J.M.,  
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20."  
 RL Nature 414:865-871(2001).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=M. mulatta; TISSUE=Hippocampus;

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OM protein - protein search, using sw model

Run on: September 16, 2003, 19:11:55 ; Search time 2.42857 Seconds  
(without alignments)  
329.187 Million cell updates/sec

Title: US-09-942-098-2\_COPY\_187\_203

Perfect score: 83  
Sequence: 1 SNKTRIDEANQRATKML 17

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt.41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	83	100.0	203 1	SN2B_CARAU
2	83	100.0	204 1	SN2A_CARAU
3	83	100.0	206 1	SN25_HUMAN
4	65	78.3	210 1	SN25_TORMA
5	46	55.4	211 1	SN23_HUMAN
6	45	54.2	212 1	SN25_DROME
7	42	50.6	83 1	MULI_PSEAE
8	42	50.6	420 1	YEO9_YEAST
9	41	49.4	494 1	PR31_YEAST
10	39	47.0	438 1	IAP1_DROME
11	39	47.0	970 1	K852_HUMAN
12	38.5	46.4	918 1	YMBB_CAEEL
13	38	45.8	151 1	STR2_RHINE
14	38	45.8	181 1	ARF2_MOUSE
15	38	45.8	294 1	CAL2_PARTE
16	38	45.8	586 1	YEMJ_ECOLI
17	37	44.6	241 1	RRPP_HRSV
18	37	44.6	241 1	RRPP_HRSV
19	37	44.6	241 1	RRPP_HRSV
20	37	44.6	329 1	YE57_MYCPN
21	37	44.6	490 1	C1KL_DROME
22	37	44.6	552 1	V664_HAEIN
23	37	44.6	885 1	ASEL_YEAST
24	37	44.6	1302 1	NRG_DROME
25	37	44.6	1755 1	PEPL_MOUSE
26	37	44.6	1769 1	YCK9_YEAST
27	37	44.6	1878 1	BRCL_CANFA
28	37	44.6	2472 1	SPCN_HUMAN
29	37	44.6	2472 1	SPCN_RAT
30	37	44.6	6669 1	NEBU_HUMAN
31	36	43.4	172 1	IPYR_SULTO
32	36	43.4	181 1	ANFI_DICDI
33	36	43.4	276 1	TABB_PSESE

34	36	43.4	433 1	HTR2_HAIVA	P42256 haloarcula
35	36	43.4	447 1	G21A_DROME	Q9VPI1 drosophila
36	36	43.4	473 1	GATB_MYCPU	Q98R09 mycoplasma
37	36	43.4	504 1	C7D8_SOYBN	Q81974 glycine max
38	36	43.4	558 1	YBAL_ECOLI	P39830 escherichia
39	36	43.4	686 1	TOP1_PYROO	Q58356 pyrococcus
40	36	43.4	693 1	SYGB_BACHD	Q9K448 bacillus ha
41	36	43.4	770 1	DBP4_YEAST	P30448 saccharomyc
42	36	43.4	829 1	GUTR_BACSU	P39143 bacillus su
43	36	43.4	847 1	DNL1_CAEEL	Q27474 caenorhabdi
44	36	43.4	887 1	QUAI_DROME	Q23989 drosophila
45	36	43.4	952 1	TOP1_STRCO	Q9X909 streptomyces

## ALIGNMENTS

```

RESULT 1
SN2B_CARAU          STANDARD:      PRT;      203 AA.
ID                  SN2B_CARAU
AC                  P36978:
DT                  01-JUN-1994 (Rel. 29, Created)
DT                  01-JUN-1994 (Rel. 29, Last sequence update)
DT                  15-SEP-2003 (Rel. 42, Last annotation update)
DE                  Synaptosomal-associated protein 25B (SNAP-25B).
OS                  SNAP-B.
OC                  Carassius auratus (Goldfish).
OC                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC                  Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC                  Cyprinidae; Carassius.
OX                  NCBI_TaxID=7957;
RN                  [1]
RP                  SEQUENCE FROM N.A.
RC                  TISSUE=Retina;
RX                  MEDLINE=94068448; PubMed=6248151;
RA                  Risinger C., Lathamar D.;
RT                  "Multiple loci for synapse protein SNAP-25 in the tetraploid
RT                  goldfish.";
RL                  Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
CC                  -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE SYNAPTIC FUNCTION OF
CC                  SPECIFIC NEURONAL SYSTEMS. ASSOCIATES WITH PROTEINS INVOLVED IN
CC                  VESICLE DOCKING AND MEMBRANE FUSION.
CC                  -1- SUBCELLULAR LOCATION: COMPLEXED WITH MACROMOLECULAR ELEMENTS OF
CC                  THE NERVE TERMINAL.
CC                  -1- TISSUE SPECIFICITY: NEURONS OF THE NEOCORTEX, HIPPOCAMPUS, AND
CC                  PERIFORM CORTEX, ANTERIOR THALAMIC NUCLEI, PONTINE NUCLEI, AND
CC                  GRANULE CELLS OF THE CEREBELLUM.
CC                  -1- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.
CC                  -1- SIMILARITY: CONTAINS 2 t-SNARE coiled-coil homology domains.
CC                  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC                  or send an email to license@sib-sib.ch).
CC                  -----
DR                  EMBL; L22976; AAA16538.1; -.
DR                  PIR; I50481; I50481.
DR                  InterPro; IPR000928; SNAP-25.
DR                  InterPro; IPR000727; T-SNARE.
DR                  Pfam; PF00835; SNAP-25; 1.
DR                  SMART; SM00357; t-SNARE; 2.
DR                  PROSITE; PS50192; T-SNARE; 2.
KW                  Synaptosome; Neurone; Repeat;
KW                  Synaptosome; Neurone; Repeat;
FT                  DOMAIN
FT                  DOMAIN 137 199
FT                  DOMAIN 85 92
FT                  CARBOHYD 77 77
FT                  CARBOHYD 185 185
FT                  SEQUENCE 203 AA; 22664 MW; 8DFBBDDBD37D6D7 CRC64;

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RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U64862; AAM69078.1; -.  
DR WormPep: ZC8.4a; CE31264.  
DR InterPro: IPR000533; Tropomyosin.  
DR PRINTS: PR00194; TROPOMIOSIN.  
KW Hypothetical protein.  
SQ SEQUENCE 2396 AA; 273873 MW; 7A184CD36D9EE3DC CRC64;

Query Match 55.4%; Score 46; DB 5; Length 2396;  
Best local similarity 60.0%; Pred. No. 81;  
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 KTRIDEANQATKML 17  
|||||:|:|  
Db 734 KTRIDELNRRVENLL 748

Search completed: September 16, 2003, 19:29:42  
Job time : 11.8182 secs

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Query Match          60.2%; Score 50; DB 11; Length 210;
Best Local Similarity 58.8%; Pred. No. 1.3;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKML 17
Db 192 TNKNRIDIANTRAKKLI 208

RESULT 13
Q9D3L3 PRELIMINARY; PRT; 221 AA.
AC Q9D3L3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Synapotosomal-associated protein, 23kD.
GN SNAP23.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arkawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojodori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Koichiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirni L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Botfield D., Boujona N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilmink L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001);
DR EMBL; AK017311; BAB30686.1; -
DR MGD; MGI:109356; Snap23.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR SMART; SM00397; t_SNARE; 2.
DR PROSITE; PS50192; T_SNARE; 2.
SQ SEQUENCE 221 AA; 24550 MW; 368862BE7233DEFB CRC64;

Query Match          60.2%; Score 50; DB 11; Length 221;
Best Local Similarity 58.8%; Pred. No. 1.4;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SNKTRIDEANORATKML 17
Db 203 TNKNRIDIANTRAKKLI 219

RESULT 14
Q95ZK3 PRELIMINARY; PRT; 2315 AA.
AC Q95ZK3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein ZC8.4b.

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GN ZC8.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Latreille P., Bradshaw H.;
RT "The sequence of C. elegans cosmid ZC8.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U64862; AAK67253.1; -
DR WormPep; ZC8.4b; CE28169.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF03915; ATP3; 1.
DR PRINTS; PF00194; TROPOMYOSIN.
SQ SEQUENCE 2315 AA; 265394 MW; 0B062E168DCD8ADE CRC64;

Query Match          55.4%; Score 46; DB 5; Length 2315;
Best Local Similarity 60.0%; Pred. No. 79;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 KTRIDEANORATKML 17
Db 626 KTRIDEANRRENNL 640

RESULT 15
Q23081 PRELIMINARY; PRT; 2396 AA.
AC Q23081;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein ZC8.4a.
GN ZC8.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Waterston R.;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Latreille P., Bradshaw H.;
RT "The sequence of C. elegans cosmid ZC8.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;

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DT 01-JUL-1997 (TREMBlrel. 04, last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, last annotation update)  
DE SNAP-25 homolog.  
OS Hirudo medicinalis (Medicinal leech).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;  
OC Aynohellicidae; Hirudiniiformes; Hirudinae; Hirudo.  
OX NCBI\_TaxID=6421;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Nerve cord;  
RX MEDLINE=97197869; PubMed=9045719;  
RA Bruns D., Engers S., Yang C., Ossig R., Jeromin A., Jahn R.;  
RT "Inhibition of transmitter release correlates with the proteolytic  
activity of tetanus toxin and botulinus toxin A in individual cultured  
cells of Hirudo medicinalis.";  
RL J. Neurosci. 17:1898-1910(1997).  
DR EMBL: U85806; AAC47499.1; -  
DR InterPro: IPR000928; SNAP-25.  
DR InterPro: IPR000727; T\_SNARE.  
DR Pfam: PF00835; SNAP-25; 1.  
DR SMART: SM00397; T\_SNARE; 2.  
DR PROSITE: PSS0192; T\_SNARE; 2.  
SQ SEQUENCE 212 AA; 23802 MW; 8FF591DF32A4FCB6 CRC64;

Query Match 63.9%; Score 53; DB 5; Length 212;  
Best Local Similarity 58.8%; Pred. No. 0.4;  
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 SSKTRIDEANORATKML 17  
ID 070377 PRELIMINARY; PRT: 210 AA.  
AC 070377;  
DT 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, last sequence update)  
DE 01-OCT-2002 (TREMBlrel. 22, last annotation update)  
DE SNAP-23.  
CN SNAP-23.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99162237; PubMed=10051443;  
RA St-Denis J.F., Cabanols J.P., Cushman S.W., Roche P.A.;  
RT "SNAP-23 participates in SNARE complex assembly in rat adipose  
cells.";  
RL Biochem. J. 338:709-715(1999).  
DR EMBL: AF052596; AAC06031.1; -  
DR InterPro: IPR000928; SNAP-25.  
DR InterPro: IPR000727; T\_SNARE.  
DR Pfam: PF00835; SNAP-25; 1.  
DR SMART: SM00397; T\_SNARE; 2.  
DR PROSITE: PSS0192; T\_SNARE; 2.  
SQ SEQUENCE 210 AA; 23235 MW; 0D63E3A6F9FE3BA2 CRC64;

Query Match 60.2%; Score 50; DB 11; Length 210;  
Best Local Similarity 58.8%; Pred. No. 1.3;  
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 SSKTRIDEANORATKML 17  
ID 070377 PRELIMINARY; PRT: 210 AA.  
AC 070377;  
DT 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, last sequence update)  
DE 01-OCT-2002 (TREMBlrel. 22, last annotation update)  
DE SNAP-23.  
CN SNAP-23.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99162237; PubMed=10051443;  
RA St-Denis J.F., Cabanols J.P., Cushman S.W., Roche P.A.;  
RT "SNAP-23 participates in SNARE complex assembly in rat adipose  
cells.";  
RL Biochem. J. 338:709-715(1999).  
DR EMBL: AF052596; AAC06031.1; -  
DR InterPro: IPR000928; SNAP-25.  
DR InterPro: IPR000727; T\_SNARE.  
DR Pfam: PF00835; SNAP-25; 1.  
DR SMART: SM00397; T\_SNARE; 2.  
DR PROSITE: PSS0192; T\_SNARE; 2.  
SQ SEQUENCE 210 AA; 23235 MW; 0D63E3A6F9FE3BA2 CRC64;

RESULT 12  
009044  
ID 009044 PRELIMINARY; PRT: 210 AA.

AC 009044;  
DT 01-JUL-1997 (TREMBlrel. 04, Created)  
DT 01-JUL-1997 (TREMBlrel. 04, last sequence update)  
DE SNAP-25 homolog.  
OS Hirudo medicinalis (Medicinal leech).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;  
OC Aynohellicidae; Hirudiniiformes; Hirudinae; Hirudo.  
OX NCBI\_TaxID=6421;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fat;  
RX MEDLINE=97312558; PubMed=9168999;  
RA Araki S., Tamori Y., Kawanishi M., Shinoda H., Masugi J., Mori H.,  
RA Niki T., Okazawa H., Kubota T., Kasuga M.;  
RT "Inhibition of the binding of SNAP-23 to syntaxin 4 by Munc18c.";  
RL Biochem. Biophys. Res. Commun. 234:257-262(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97220227; PubMed=9067602;  
RA Wang G., Wilkin J.W., Hao G., Bankaitis V.A., Scherer P.E.,  
RA Baldini G.;  
RT "SynDET is a novel SNAP-25 related protein expressed in many  
tissues.";  
RL J. Cell Sci. 110:505-513(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX STRAIN=129/SVJ;  
RA Valyanaathan V.V., Roche P.A.;  
RT "Structure and chromosomal localization of the mouse SNAP-23 gene.";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Embryo;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuo H.A., Ashburner M., Batilov S., Casavant T.,  
RA Felschmann W., Gaasterland T., Glasi C., King B., Kochiya H.,  
RA Kuenl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Kombearts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilting L.,  
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
DR EMBL: AB000822; BAA20345.1; -  
DR EMBL: U73143; AAB53597.1; -  
DR EMBL: AF213257; AAF23503.1; -  
DR EMBL: AF213251; AAF23503.1; JOINED.  
DR EMBL: AF213252; AAF23503.1; JOINED.  
DR EMBL: AF213253; AAF23503.1; JOINED.  
DR EMBL: AF213254; AAF23503.1; JOINED.  
DR EMBL: AF213255; AAF23503.1; JOINED.  
DR EMBL: AF213256; AAF23503.1; JOINED.  
DR EMBL: AK019162; BAB31577.1; -  
DR WGI:109356; Snap23.  
DR InterPro: IPR000928; SNAP-25.  
DR InterPro: IPR000727; T\_SNARE.  
DR Pfam: PF00835; SNAP-25; 1.  
DR SMART: SM00397; T\_SNARE; 2.  
DR PROSITE: PSS0192; T\_SNARE; 2.  
SQ SEQUENCE 210 AA; 23261 MW; 6919E127E16BA2C9 CRC64;

QY 1 SNKTRIDEANORATKML 17  
|||||  
Db 187 SNKTRIDEANORATKML 203

## RESULT 6

Q8AXM2 PRELIMINARY; PRT; 206 AA.  
AC Q8AXM2;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE SNAP23a.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kolk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF335586; AAO13788.1; -  
SQ SEQUENCE 206 AA; 23122 MW; 2D1D0FD35E0C1DDF CRC64;

Query Match 83.1%; Score 69; DB 13; Length 206;  
Best Local Similarity 82.4%; Pred. No. 0.00068;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKML 17  
||| |||||  
Db 187 SNKTRIDEANORATKML 203

## RESULT 7

Q8AXM1 PRELIMINARY; PRT; 206 AA.  
AC Q8AXM1;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE SNAP23b.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kolk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF335587; AAO13789.1; -  
SQ SEQUENCE 206 AA; 23187 MW; 7D3B20717E577F02 CRC64;

Query Match 83.1%; Score 69; DB 13; Length 206;  
Best Local Similarity 82.4%; Pred. No. 0.00068;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKML 17  
||| |||||  
Db 187 SNKTRIDEANORATKML 203

## RESULT 8

Q8T3S4 PRELIMINARY; PRT; 212 AA.  
ID Q8T3S4;  
DT 01-JUN-2002 (TREMBlrel. 21, Created)  
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE SNAP25 fusion protein.  
OS Loligo pealeii (Longfin squid).

OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
OC Decapodiformes; Loliginidae; Loligo.  
OX NCBI\_TaxID=6621;  
RN [1]

RP SEQUENCE FROM N.A.  
RA Bracher A., Kadlec J., Betz H., Weissenhorn W.;  
RL "X-ray structure of a neuronal complexin/SNARE complex from squid.";  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Dresbach T., O'Connor V., Burns M., Augustine G., Betz H.;  
RL "Squid SNAP25.";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY092757; AAM18191.1; -  
DR InterPro: IPR000928; SNAP-25.  
DR InterPro: IPR000727; T\_SNARE.  
DR Pfam: PF00835; SNAP-25; 1.  
DR SMART: SM00397; T\_SNARE; 2.  
DR PROSITE: PS50192; T\_SNARE; 2.  
SQ SEQUENCE 212 AA; 23816 MW; 127601619DE79E2D CRC64;

Query Match 78.3%; Score 65; DB 5; Length 212;  
Best Local Similarity 70.6%; Pred. No. 0.0034;  
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKML 17  
||| |||||  
Db 194 SNKTRIDEANORATKML 210

## RESULT 9

Q8J1S7 PRELIMINARY; PRT; 204 AA.  
AC Q8J1S7;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE SNAP-23.  
GN XOSNAP-23.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mashima J., Nagahama M., Hatsuzawa K., Tani K., Kikuchi F.,  
RA Horigome T., Yamamoto A., Tagaya M.;  
RL "Evidence for the involvement of alpha-SNAP and SNAP-23 in the fusion  
of nuclear membrane vesicles.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB033718; BAC06591.1; -  
DR InterPro: IPR000928; SNAP-25.  
DR InterPro: IPR000727; T\_SNARE.  
DR Pfam: PF00835; SNAP-25; 1.  
DR SMART: SM00397; T\_SNARE; 2.  
DR PROSITE: PS50192; T\_SNARE; 2.  
SQ SEQUENCE 204 AA; 22771 MW; D034F75E638E805 CRC64;

Query Match 72.3%; Score 60; DB 13; Length 204;  
Best Local Similarity 64.7%; Pred. No. 0.024;  
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKML 17  
:|||||||:|:|:  
Db 187 SNKTRIDEANORATKML 203

## RESULT 10

ID Q01389 PRELIMINARY; PRT; 212 AA.  
AC Q01389;  
DT 01-JUL-1997 (TREMBlrel. 04, Created)

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DT      01-NOV-1998 (TREMBLER, 08, last sequence update)
DR      01-OCN-2002 (TREMBLER, 22, last annotation update)
DE      Synaprosome-associated protein 25.1 (Fragment).
GN      SNAP25A OR SNAP.
OS      Brachydanio rerio (zebrafish) (Danio rerio).
OC      Euryptera; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
CC      Cyprinidae; Danio.
OX      NCBI_TaxId=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=99057281; Pubmed=9843147;
RA      R. Ringer C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
RT      Lathammar D.;
RT      "Cloning of two loci for synapse protein Snap25 in zebrafish:
RT      comparison of paralogous linkage groups suggests loss of one locus in
RT      the mammalian lineage."
RL      J. Neurosci. Res. 54:563-573(1998).
DR      EMBL: AF091593; AAC64289.1; -
DR      ZFIN: ZDB-GENE-980526-468; snap25a.
DR      InterPro: IPR000928; SNAP-25.
DR      InterPro: IPR000727; T_SNARE.
DR      Pfam: PF00835; SNAP-25; 1.
DR      SMART: SM00397; T_SNARE; 1.
DR      PROSITE: PSS0192; T_SNARE; 1.
FT      NON_TER
SQ      SEQUENCE 124 AA; 13616 MW; 50E27DBDB33D958C CRC64;

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	Query Match	100.0%	Score 83;	DB 13;	Length 124;
	Best Local Similarity	100.0%	Pred. No. 1.5e-05;		
Matches	17;	Conservative	0;	Mismatches	0;
				Indels	0;
Qy	1	SNKTRIDEANORATKML	17		
Db	105	SNKTRIDEANORATKML	121		

RESULT 3	09GM34	PRELIMINARY;	PRT;	143 AA.
AC	09GM34;			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, last annotation update)			
DE	Hypothetical 16.0 kDa protein.			
OS	Macaca fascicularis (Crab eating macaque) (Cynomolus monkey).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Primates; Catarrhini; Cercopithecoidea;			
CC	Cercopitheciinae; Macaca.			
OX	NCBI_Taxid=9541;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RA	Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,			
RA	Suzuki Y., Sugano S., Hashimoto K.;			
RT	"Isolation of full-length cDNA clones from macaque brain cDNA			
RL	libraries."			
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB049852; BAB16738.1; -			
DR	InterPro; IPR000928; SNAP-25.			
DR	InterPro; IPR000727; T_SNARE.			
DR	Pfam; PF00835; SNAP-25; 1.			
DR	SMART; SM00397; t_SNARE; 1.			
DR	PROSITE; PSS0192; T_SNARE; 1.			
DR	Hypothetical protein.			
SQ	SEQUENCE 143 AA; 16043 MW; D625DBAAA0893F7B0 CRC64;			

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Query Match      100.0%; Score 83; DB 6; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 SNKTRIDEANORATKML 17
|||||

```

Db 124 SNKTRIDEANORATKML 140

RESULT 4		PRELIMINARY;		PRT;		203 AA.	
Q93579	093579						
AC	093579;						
DT	01-NOV-1998 (TREMBLrel. 08, Created)						
DT	01-NOV-1998 (TREMBLrel. 08, last sequence update)						
DT	01-OCT-2002 (TREMBLrel. 22, last annotation update)						
DE	SYNAPPOsome-associated protein 25.2 (SYNAPPOsome associated protein 25.2).						
GN	SNAP25B OR SNAP.						
OS	Brachydanio rerio (zebrafish) (Danio rerio).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Cyprinodonteygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;						
OC	Cyprinidae; Danio.						
OX	NCBI_TaxID=7955;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RA	Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,						
RT	Lachmann D.;						
RT	Cloning of two loci for synapse protein Snap25 in zebrafish;						
RT	comparison of paralogous lineage groups suggests loss of one locus in						
RT	the mammalian lineage.;						
RL	J. Neurosci. Res. 0:0-0(1998).						
DR	EMBL; AF091594; AAC64290.1; -						
DR	EMBL; AF091596; AAC73007.1; -						
DR	ZFIN; ZDB-GENE-980526-392; snap25b.						
DR	InterPro; IPR000928; SNAP-25.						
DR	InterPro; IPR000727; T-SNARE.						
DR	Pfam; PF00835; SNAP-25; 1.						
DR	SMART; SM00357; T-SNARE; 2.						
DR	PROSITE; PS50192; T-SNARE; 2.						
QO	SEQUENCE 203 AA; 22647 MW; 93B759DDDC93F38 CRC64;						

Query Match	100.0%;	Score 83;	DB 13;	Length 203;
Best Local Similarity	100.0%;	Pred. No. 2.6e-06;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

Query Match	100.0%	Score 83;	DB 4;	Length 206;
Best Local Similarity	100.0%;	Pred. No. 2.6e-06;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0.

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 16, 2003, 19:21:26 ; Search time 10.8182 Seconds  
(without alignments)  
405.511 Million cell updates/sec

Title: US-09-942-098-2\_COPY\_187\_203  
Perfect score: 83  
Sequence: 1 SNKTRIDEANORATKML 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rotent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	80	4 Q9BR45	Q9BR45 homo sapien
2	83	100.0	124	13 Q93578	Q93578 Brachydanio
3	83	100.0	143	6 Q9GM34	Q9GM34 macaca fasc
4	83	100.0	203	13 Q93579	Q93579 brachydanio
5	83	100.0	206	4 Q96FM2	Q96FM2 homo sapien
6	69	83.1	206	13 Q8AXM2	Q8AXM2 xenopus lae
7	69	83.1	206	13 Q8AXM1	Q8AXM1 xenopus lae
8	65	78.3	212	5 Q8T3S4	Q8T3S4 loligo peal
9	60	72.3	204	13 Q8J1S7	Q8J1S7 xenopus lae
10	53	63.9	212	5 O01389	O01389 hitudo medi
11	50	60.2	210	11 Q70377	Q70377 rattus norv
12	50	60.2	210	11 Q09044	Q09044 mus musculu
13	50	60.2	221	11 Q9D3L3	Q9D3L3 mus musculu
14	46	55.4	2315	5 Q95ZK3	Q95ZK3 caenorhabdi
15	46	55.4	2396	5 Q23081	Q23081 caenorhabdi
16	45	54.2	83	2 Q85440	Q85440 pseudomonas

17	45	54.2	83	2 Q85439	Q85439 pseudomonas
18	45	54.2	83	2 Q85431	Q85431 pseudomonas
19	45	54.2	125	5 Q96576	Q96576 leucophaea
20	45	54.2	210	11 Q35620	Q35620 mus musculu
21	44.5	53.6	191	17 Q8Z772	Q8Z772 pyrobaculum
22	44	53.0	90	5 Q96578	Q96578 leucophaea
23	44	53.0	207	5 Q62414	Q62414 caenorhabdi
24	44	53.0	530	4 Q9BWU6	Q9BWU6 homo sapien
25	44	53.0	573	4 Q9HBY5	Q9HBY5 homo sapien
26	44	53.0	1313	4 Q9HCK7	Q9HCK7 homo sapien
27	44	53.0	2029	4 Q9C014	Q9C014 homo sapien
28	44	53.0	2069	4 Q9C013	Q9C013 homo sapien
29	44	53.0	2073	4 Q9C012	Q9C012 homo sapien
30	44	53.0	2090	4 Q9HAT7	Q9HAT7 homo sapien
31	44	53.0	2096	4 Q9UH61	Q9UH61 homo sapien
32	43.5	52.4	55	4 Q8NCR8	Q8NCR8 homo sapien
33	43	51.8	353	16 Q8FNU8	Q8FNU8 corynebacte
34	43	51.8	771	5 Q9XZJ3	Q9XZJ3 dictyostell
35	42	50.6	83	2 Q85420	Q85420 pseudomonas
36	42	50.6	83	2 Q85434	Q85434 pseudomonas
37	42	50.6	83	2 Q85437	Q85437 pseudomonas
38	42	50.6	83	2 Q85441	Q85441 pseudomonas
39	42	50.6	83	2 Q85418	Q85418 pseudomonas
40	42	50.6	83	2 Q85433	Q85433 pseudomonas
41	42	50.6	83	2 Q85438	Q85438 pseudomonas
42	42	50.6	83	2 Q85423	Q85423 pseudomonas
43	42	50.6	83	2 Q85435	Q85435 pseudomonas
44	42	50.6	83	2 Q85410	Q85410 pseudomonas
45	42	50.6	83	2 Q85413	Q85413 pseudomonas

#### ALIGNMENTS

##### RESULT 1

Q9BR45 PRELIMINARY; PRT; 80 AA.  
ID Q9BR45  
AC Q9BR45;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE D11068F16.2.2 (Novel protein (Isoform 2)).  
OS SNAF25.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Babpage A.;  
RU Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL, AL023913; CAC34535.1..  
DR InterPro; IPR000928; SNAF-25.  
DR InterPro; IPR000727; T\_SNAF.  
DR Pfam; PF00835; SNAF-25; 1.  
DR SMART; SM00397; t\_SNAF; 1.  
DR PROSITE; PSS0192; T\_SNAF; 1.  
SQ SEQUENCE 80 AA; 8993 MW; A120C65714D9F071 CRC64;

Query Match 100.0%; Score 83; DB 4; Length 80;  
Best Local Similarity 100.0%; Pred. No. 9.7e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SNKTRIDEANORATKML 17  
DB 61 SNKTRIDEANORATKML 77

RESULT 2  
ID Q93578 PRELIMINARY; PRT; 124 AA.  
AC Q93578;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)





```

: SOFTWARE: Fastseq for Windows Version 4.0.
: SEQ ID NO 15
: LENGTH: 212
: TYPE: prt
: ORGANISM: Strongylocentrotus purpuratus
US-03-942-098-15

```

query Match	59.8%;	Score 627;	DB 12;	Length 212;
Best Local Similarity	61.8%;	Pred. No. 4e-51;		
Matches 126;	Conservative 29;	Mismatches 45;	Indels 4;	Gaps 2

[illegible]

Dy 64 MDQINIKDMEAEKNIITDLGFCGCVCPCNKL---KSSDAKKAKWAGNNQDVVAS-QPAR 119  
||| ||| : ||| | : ||| | ||| ||| |||  
Db 66 MDQINTDMBAEKENLTGLEKCCGICVCPWKLLGNFPEKGDDYKKTTWGNDGDGVNSHQPMR 125

QY 120 VDEREQMAISGGFTRVTNDARENMEDENLEQVSSIGLNLRHMLDMGNEIDTQNRQID 179

Db 126 MEDDRDCGGNASMITRITNDAREMDEMLTQVSSIVGNLRHMAIDMQSEICAGQNSQVG 185

```
QY      180 RIMEKADSNKTRIDEANQRA TKML 203
        || ||||: ||: ||||: |
DB      186 RITSKAESNEGRINSADKRAKNIL 209
```

RESULT 13  
US-09-942-024-13  
Sequence 13 Application file 00000000

```

; Publication No. US20030143650A1
;
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas Ector

```

```

; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; TITLE OF INVENTION: Serotype A/E Toxins
; FILING REFERENCE: P-AB 4803

```

```

;
; CURRENT APPLICATION NUMBER: US/09/942,022
;
; CURRENT FILING DATE: 2001-08-28
;
; NUMBER OF SEQ ID NOS: 96
;
; SOFTWARE: FastSeq for Windows Version 4.0

```

```

; SEQ ID NO 13
;
; LENGTH: 212
;
; TYPE: PRT
;
; ORGANISM: Drosophila su

```

US-09-942-024-13	Query Match	59.08;	Score 618.5;	DB 12;	Length 212;
	Best local similarity	62.08	Prod	NO. 2	Score 50

Matches	124;	Mismatches	43;	Indels	1;	Gaps	1
Qy	8	RNECEMORADADESL	ESTRMLQTYEESKAGIRTVMLDPOGEOLRIEESMDOI	67			

15 KTELEELTOINAOGVADESLESTRIRNALALCEESKEENGIRTLVALDPOGEOJDRIEEGMDJ 74

D6

68 NKDMEAEKNLTJDKGFCGJCVCNCNKLKSSDAYKAKGANNQD--VVASOPARYDEREQ 126

Oy

D5 /5 NADNRKAEAKNLSGMEKCCGICVLPCMKSSQSRKEDDGTWKGGDDGKVVNNQPRVMDRRNG 134

OY 127 MAISGGFIRVTNDARENEMDENTLEOVSGIIGNLRHMAIDMGNEIDPTQNRQIDRIKEMAD 1866

DB 135 MNAQAGY IGRITNDAREDEMEENMGVNTMIGNLRNALDNGSELEQNQRQIDRINKRGE 194  
QY 187 SNKTRIDEANQRATKML 203  
||: || |||| ...||

DB 195 SNEARLAVANQRAHQLL 211

US-09-942-098-13  
; Sequence 13, Application US/09942098

```

: Publication No. US20030114651A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Steward, Iance E.
:
: APPLICANT: Fernandez-Salas, Ester
:
: APPLICANT: Aoki, Kei Roger
:
: TITLE OF INVENTION: Fret Protease Assays For Clostridia)

```

```

; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28

```

```

; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 13
; LENGTH: 212
;

```

ORGANISM: *Drosophila* sp  
US-09-942-098-13

Best Local Similarity - 62.9%; Pred. No. 2.5e-50;  
Matches 124; Conservative 29; Mismatches 43; Indels 1; Gaps 1

15 KTELEELQINAGVADESLESTRMLALCESEKNGIRTLVALDPGGEQLTRIEGMDQI 74

D5 127 MATCCGCTBBYENDADPENNDENDENTFOVCGCTTCATBHMATDWCNETMTONBOPTDITMEKAD16

135 MAAQAGYIGRITNDAREDEMEENMGQVNTMGLRNALDMGSELENNQRQIDIRNRKE 194

Db 195 SNEARIAVANQRAHQLL 211

RESULT 15  
US-09-925-300-1718  
; Sequence 1718, Application US/09925300  
; Patent No. 7530030, 7516811

```

; GENERAL INFORMATION:
;
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

```

```

; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05088

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; PRIOR FILING DATE: 2000-03-08  
 ; PRIOR APPLICATION NUMBER: 60/124,270  
 ; PRIOR FILING DATE: 1999-03-12  
 ; NUMBER OF SEQ ID NOS: 1890

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1718
; LENGTH: 213
; TYPE: DMT

```

US-09-925-300-1718  
ORGANISM: Homo sapiens  
Query Match

Best Local Similarity 60.5%; Pred. NO. 1.8e-49;  
Matches 124; Conservative 29; Mismatches 41; Indels 11; Gaps 3

```

72 KRAEKNITDILGKEGCIJCVCPCNKIK---SSDAYKKAWS-----NNODGVWASQPARVYDER 121
Db 9 EEIOGRAHQITDESLESTRILGLAIESODAGIKTITMLDEQKEQINRIEESLDQINKDM 60

```

D6 69 REYEKTLTEINKCCGLCVPCNRIKNEESGAKYKTTWGGGGENSPCNVVSQDPVYINGQ 128

QY 181 IMEKADSNKTRIDEANORATKMLGSG 206  
Db 178 IMDMADSNKTRIDEANORATKMLGSG 203

## RESULT 9

US-09-942-024-16  
; Sequence 16, Application US/09942024  
; Publication No. US20030143650A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
; FILE REFERENCE: P-AR 4803  
; CURRENT APPLICATION NUMBER: US/09/942,024  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 249  
; TYPE: PRF  
; ORGANISM: Gallus gallus  
US-09-942-024-16

Query Match 85.4%; Score 895; DB 12; Length 249;  
Best Local Similarity 95.1%; Pred. No. 3.5e-76;  
Matches 175; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAEDADMNELEEMORRADQDLADESLESTRMLQLVESKDGIRTLVLMDEQGOLERI 60  
Db 1 MAEDADMNELEEMORRADQDLADESLESTRMLQLVESKDGIRTLVLMDEQGOLDRV 60  
QY 61 EEGMOQINNDKMEAEKNLTDLGKFCGCLCPCKNLKSSPAYKKANGNNDGVVASOPARV 120  
Db 61 EEGMHHINDDKMEAEKNLTDLGKCGCLFCPCNKLKSSPAYKKANGNNDGVVASOPARV 120  
QY 121 VDEREOMASISGCFIRRYTNDARENMENDENLEOVSGIIGNLRHMLDMGNEIDTONROIDR 180  
Db 121 VDEREOMASISGCFIRRYTNDARENMENDENLEOVSGIIGNLRHMLDMGNEIDTONROIDR 180  
QY 181 IMEK 184  
Db 181 IMEK 184

## RESULT 10

US-09-942-098-16  
; Sequence 16, Application US/09942098  
; Publication No. US20030143651A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Clostridia  
; FILE REFERENCE: P-AR 4802  
; CURRENT APPLICATION NUMBER: US/09/942,098  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 249  
; TYPE: PRF  
; ORGANISM: Gallus gallus  
US-09-942-098-16

Query Match 85.4%; Score 895; DB 12; Length 249;  
Best Local Similarity 95.1%; Pred. No. 3.5e-76;  
Matches 175; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAEDADMNELEEMORRADQDLADESLESTRMLQLVESKDGIRTLVLMDEQGOLERI 60  
Db 1 MAEDADMNELEEMORRADQDLADESLESTRMLQLVESKDGIRTLVLMDEQGOLDRV 60  
QY 61 EEGMOQINNDKMEAEKNLTDLGKFCGCLCPCKNLKSSPAYKKANGNNDGVVASOPARV 120  
Db 61 EEGMHHINDDKMEAEKNLTDLGKCGCLFCPCNKLKSSPAYKKANGNNDGVVASOPARV 120  
QY 121 VDEREOMASISGCFIRRYTNDARENMENDENLEOVSGIIGNLRHMLDMGNEIDTONROIDR 180  
Db 121 VDEREOMASISGCFIRRYTNDARENMENDENLEOVSGIIGNLRHMLDMGNEIDTONROIDR 180  
QY 181 IMEK 184  
Db 181 IMEK 184

## RESULT 11

US-09-942-024-15  
; Sequence 15, Application US/09942024  
; Publication No. US20030143650A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
; FILE REFERENCE: P-AR 4803  
; CURRENT APPLICATION NUMBER: US/09/942,024  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 212  
; TYPE: PRF  
; ORGANISM: Strongylocentrotus purpuratus  
US-09-942-024-15

Query Match 59.8%; Score 627; DB 12; Length 212;  
Best Local Similarity 61.8%; Pred. No. 4e-51;  
Matches 126; Conservative 29; Mismatches 45; Indels 4; Gaps 2;

QY 4 DADMNELEEMORRADQDLADESLESTRMLQLVESKDGIRTLVLMDEQGOLERIEG 63  
Db 6 DMMRSELEIOMOSMTDESLESTRMLQVAESODMGITLVLMDEQGOLDRIEG 65  
QY 64 MDQINKMEAEKNLTDLGKFCGCLCPCKNLKSSPAYKKANGNNDGVVASOPARV 119  
Db 64 MDQINTDMKEAEKNLTDLGKCGCLFCPCNKLKSSPAYKKANGNNDGVVASOPARV 125  
QY 120 VDEREOMASISGCFIRRYTNDARENMENDENLEOVSGIIGNLRHMLDMGNEIDTONROIDR 179  
Db 126 MEDDDGCGGNSMTIRITNDARENMENDENLEOVSGIIGNLRHMLDMGNEIDTONROIDR 185  
QY 180 RIMEKADSNKTRIDEANORATKML 203  
Db 186 RITSKAESNEGRINSADKRAKNIL 209

## RESULT 12

US-09-942-098-15  
; Sequence 15, Application US/09942098  
; Publication No. US20030143651A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Clostridia  
; FILE REFERENCE: P-AR 4802  
; CURRENT APPLICATION NUMBER: US/09/942,098  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96

LENGTH: 206  
TYPE: PRT  
ORGANISM: Rattus sp.  
US-09-942-098-7

Query Match 100.0%; Score 1048; DB 12; Length 206;  
Best Local Similarity 100.0%; Pred. No. 1.2e-90;  
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEDADNRNELEEMQRRADOLADESLESTRMLQLVESKDGAGIRTLVMLDEQGEOLERI 60  
DB 1 MAEDADNRNELEEMQRRADOLADESLESTRMLQLVESKDGAGIRTLVMLDEQGEOLERI 60  
QY 61 EEGMDQINKDMKEAKENLTDGKFCGLVCPCNKLKSSDAYKKAGNNQDGVVASOPARV 120  
DB 61 EEGMDQINKDMKEAKENLTDGKFCGLVCPCNKLKSSDAYKKAGNNQDGVVASOPARV 120  
QY 121 VDREQMAISGCFIRRYTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTONROIDR 180  
DB 121 VDREQMAISGCFIRRYTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTONROIDR 180  
QY 181 IMEKADSNKTRIDEANORATKMLGSG 206  
DB 181 IMEKADSNKTRIDEANORATKMLGSG 206

## RESULT 6

US-09-942-098-12  
Sequence 12, Application US/09942098  
Publication No. US20030143651A1  
GENERAL INFORMATION:  
APPLICANT: Steward, Lance E.  
APPLICANT: Fernandez-Salas, Ester  
APPLICANT: Aoki, Kei Roger  
TITLE OF INVENTION: Fret Protease Assays For Clostridial  
TITLE OF INVENTION: Toxins  
FILE REFERENCE: P-AR 4802  
CURRENT APPLICATION NUMBER: US/09/942, 098  
CURRENT FILING DATE: 2001-08-28  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 206  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-942-098-12

Query Match 100.0%; Score 1048; DB 12; Length 206;  
Best Local Similarity 100.0%; Pred. No. 1.2e-90;  
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEDADNRNELEEMQRRADOLADESLESTRMLQLVESKDGAGIRTLVMLDEQGEOLERI 60  
DB 1 MAEDADNRNELEEMQRRADOLADESLESTRMLQLVESKDGAGIRTLVMLDEQGEOLERI 60  
QY 61 EEGMDQINKDMKEAKENLTDGKFCGLVCPCNKLKSSDAYKKAGNNQDGVVASOPARV 120  
DB 61 EEGMDQINKDMKEAKENLTDGKFCGLVCPCNKLKSSDAYKKAGNNQDGVVASOPARV 120  
QY 121 VDREQMAISGCFIRRYTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTONROIDR 180  
DB 121 VDREQMAISGCFIRRYTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTONROIDR 180  
QY 181 IMEKADSNKTRIDEANORATKMLGSG 206  
DB 181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 7  
US-09-942-024-14  
Sequence 14, Application US/09942024  
Publication No. US20030143650A1  
GENERAL INFORMATION:

APPLICANT: Steward, Lance E.  
APPLICANT: Fernandez-Salas, Ester  
APPLICANT: Aoki, Kei Roger  
TITLE OF INVENTION: Fret Protease Assays For Botulinum  
TITLE OF INVENTION: Serotype A/E Toxins  
FILE REFERENCE: P-AR 4803  
CURRENT APPLICATION NUMBER: US/09/942, 024  
CURRENT FILING DATE: 2001-08-28  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14  
LENGTH: 203  
TYPE: PRT  
ORGANISM: Carassius auratus  
US-09-942-024-14

Query Match 89.1%; Score 933.5; DB 12; Length 203;  
Best Local Similarity 89.3%; Pred. No. 6.5e-80;  
Matches 184; Conservative 7; Mismatches 12; Indels 3; Gaps 1;

QY 1 MAEDADNRNELEEMQRRADOLADESLESTRMLQLVESKDGAGIRTLVMLDEQGEOLERI 60  
DB 1 MAEDADNRNELEEMQRRADOLADESLESTRMLQLVESKDGAGIRTLVMLDEQGEOLERI 60  
QY 61 EEGMDQINKDMKEAKENLTDGKFCGLVCPCNKLKSSDAYKKAGNNQDGVVASOPARV 120  
DB 61 EEGMDQINKDMKEAKENLTDGKFCGLVCPCNKLKSSDAYKKAGNNQDGVVASOPARV 117  
QY 121 VDREQMAISGCFIRRYTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTONROIDR 180  
DB 118 VDREQMAISGCFIRRYTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTONROIDR 177  
QY 181 IMEKADSNKTRIDEANORATKMLGSG 206  
DB 178 IMEKADSNKTRIDEANORATKMLGSG 203

## RESULT 8

US-09-942-098-14  
Sequence 14, Application US/09942098  
Publication No. US20030143651A1  
GENERAL INFORMATION:  
APPLICANT: Steward, Lance E.  
APPLICANT: Fernandez-Salas, Ester  
APPLICANT: Aoki, Kei Roger  
TITLE OF INVENTION: Fret Protease Assays For Clostridial  
TITLE OF INVENTION: Toxins  
FILE REFERENCE: P-AR 4802  
CURRENT APPLICATION NUMBER: US/09/942, 098  
CURRENT FILING DATE: 2001-08-28  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14  
LENGTH: 203  
TYPE: PRT  
ORGANISM: Carassius auratus  
US-09-942-098-14

Query Match 89.1%; Score 933.5; DB 12; Length 203;  
Best Local Similarity 89.3%; Pred. No. 6.5e-80;  
Matches 184; Conservative 7; Mismatches 12; Indels 3; Gaps 1;

QY 1 MAEDADNRNELEEMQRRADOLADESLESTRMLQLVESKDGAGIRTLVMLDEQGEOLERI 60  
DB 1 MAEDADNRNELEEMQRRADOLADESLESTRMLQLVESKDGAGIRTLVMLDEQGEOLERI 60  
QY 61 EEGMDQINKDMKEAKENLTDGKFCGLVCPCNKLKSSDAYKKAGNNQDGVVASOPARV 120  
DB 61 EEGMDQINKDMKEAKENLTDGKFCGLVCPCNKLKSSDAYKKAGNNQDGVVASOPARV 117  
QY 121 VDREQMAISGCFIRRYTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTONROIDR 180  
DB 118 VDREQMAISGCFIRRYTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTONROIDR 177

Db 181 IMEKADSNKTRIDEANORATKMLGSG 206

## RESULT 2

US-09-942-024-7  
; Sequence 7, Application US/09942024  
; Publication No. US20030143650A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
; FILE REFERENCE: P-AR 4803  
; CURRENT APPLICATION NUMBER: US/09/942,024  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 206  
; TYPE: PRF  
; ORGANISM: Rattus sp.  
US-09-942-024-7

Query Match 100.0%; Score 1048; DB 12; Length 206;  
Best Local Similarity 100.0%; Pred. No. 1.2e-90;  
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAEDADMRELEEMORRADQDLADESLESTRMLQVVEESKDAGITVLWLDGEGQLERI 60

Db 1 MAEDADMRELEEMORRADQDLADESLESTRMLQVVEESKDAGITVLWLDGEGQLERI 60

Qy 61 EEGMDQINKDMKEAEKNLTDLGKFCGLCYCPCKNLKSSDAYKKANGNODGVVASQPARV 120

Db 61 EEGMDQINKDMKEAEKNLTDLGKFCGLCYCPCKNLKSSDAYKKANGNODGVVASQPARV 120

Qy 121 VDERQOMASISGFIIRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR 180

Db 121 VDERQOMASISGFIIRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR 180

Qy 181 IMEKADSNKTRIDEANORATKMLGSG 206

Db 181 IMEKADSNKTRIDEANORATKMLGSG 206

## RESULT 3

US-09-942-024-12  
; Sequence 12, Application US/09942024  
; Publication No. US20030143650A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
; FILE REFERENCE: P-AR 4803  
; CURRENT APPLICATION NUMBER: US/09/942,024  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 206  
; TYPE: PRF  
; ORGANISM: Mus musculus  
US-09-942-024-12

Query Match 100.0%; Score 1048; DB 12; Length 206;  
Best Local Similarity 100.0%; Pred. No. 1.2e-90;  
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAEDADMRELEEMORRADQDLADESLESTRMLQVVEESKDAGITVLWLDGEGQLERI 60

Db 1 MAEDADMRELEEMORRADQDLADESLESTRMLQVVEESKDAGITVLWLDGEGQLERI 60

Qy 61 EEGMDQINKDMKEAEKNLTDLGKFCGLCYCPCKNLKSSDAYKKANGNODGVVASQPARV 120

Db 61 EEGMDQINKDMKEAEKNLTDLGKFCGLCYCPCKNLKSSDAYKKANGNODGVVASQPARV 120

Qy 121 VDERQOMASISGFIIRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR 180

Db 121 VDERQOMASISGFIIRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR 180

Qy 181 IMEKADSNKTRIDEANORATKMLGSG 206

Db 181 IMEKADSNKTRIDEANORATKMLGSG 206

## RESULT 4

US-09-942-098-2  
; Sequence 2, Application US/09942098  
; Publication No. US20030143651A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; TITLE OF INVENTION: Fret Protease Assays For Clostridial  
; FILE REFERENCE: Toxins  
; CURRENT APPLICATION NUMBER: US/09/942,098  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 206  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-09-942-098-2

Query Match 100.0%; Score 1048; DB 12; Length 206;  
Best Local Similarity 100.0%; Pred. No. 1.2e-90;  
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAEDADMRELEEMORRADQDLADESLESTRMLQVVEESKDAGITVLWLDGEGQLERI 60

Db 1 MAEDADMRELEEMORRADQDLADESLESTRMLQVVEESKDAGITVLWLDGEGQLERI 60

Qy 61 EEGMDQINKDMKEAEKNLTDLGKFCGLCYCPCKNLKSSDAYKKANGNODGVVASQPARV 120

Db 61 EEGMDQINKDMKEAEKNLTDLGKFCGLCYCPCKNLKSSDAYKKANGNODGVVASQPARV 120

Qy 121 VDERQOMASISGFIIRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR 180

Db 121 VDERQOMASISGFIIRVTNDARENEMDENLEQVSGIIGNLRHMALDMGNEIDTQNRQIDR 180

Qy 181 IMEKADSNKTRIDEANORATKMLGSG 206

Db 181 IMEKADSNKTRIDEANORATKMLGSG 206

## RESULT 5

US-09-942-098-7  
; Sequence 7, Application US/09942098  
; Publication No. US20030143651A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; TITLE OF INVENTION: Fret Protease Assays For Clostridial  
; FILE REFERENCE: Toxins  
; CURRENT APPLICATION NUMBER: US/09/942,098  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 16, 2003, 19:23:56 ; Search time 53.5065 Seconds  
(without alignments)  
573.239 Million cell updates/sec

Title: US-09-942-098-2  
1048  
Sequence: 1 MAEDADMRNELEEMQRRADQ.....SNKTRIDEANQATKMLGSG 206

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 556269 seqs, 148893369 residues  
Total number of hits satisfying chosen parameters: 556269

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCR\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCITUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1048	100.0	206	12	US-09-942-024-2
2	1048	100.0	206	12	US-09-942-024-7
3	1048	100.0	206	12	US-09-942-024-12
4	1048	100.0	206	12	US-09-942-098-2
5	1048	100.0	206	12	US-09-942-098-7
6	1048	100.0	206	12	US-09-942-098-12
7	933.5	89.1	203	12	US-09-942-024-14
8	933.5	89.1	203	12	US-09-942-098-14
9	895	85.4	249	12	US-09-942-024-16
10	895	85.4	249	12	US-09-942-098-16
11	627	59.8	212	12	US-09-942-024-15
12	627	59.8	212	12	US-09-942-098-15
13	618.5	59.0	212	12	US-09-942-024-13
14	618.5	59.0	212	12	US-09-942-098-13
15	609.5	58.2	213	10	US-09-925-300-1718

16	578	55.2	116	11	US-09-962-3608-11	Sequence 11, Appl
17	572	54.6	116	11	US-09-962-3608-12	Sequence 12, Appl
18	361.5	34.5	129	9	US-09-925-299-1245	Sequence 1245, Ap
19	361.5	34.5	129	11	US-09-925-299-1245	Sequence 1245, Ap
20	244	23.3	49	9	US-09-864-761-43057	Sequence 43057, A
21	230	21.9	300	9	US-09-952-689-9	Sequence 9, Appl1
22	197.5	18.8	284	9	US-09-952-689-3	Sequence 3, Appl1
23	183.5	17.5	283	9	US-09-952-689-5	Sequence 5, Appl1
24	164	15.6	33	12	US-09-942-024-33	Sequence 33, Appl
25	164	15.6	33	12	US-09-942-024-33	Sequence 38, Appl
26	164	15.6	33	12	US-09-942-098-33	Sequence 33, Appl
27	164	15.6	33	12	US-09-942-098-38	Sequence 38, Appl
28	155	14.8	33	12	US-09-942-024-37	Sequence 37, Appl
29	155	14.8	33	12	US-09-942-098-37	Sequence 37, Appl
30	155	14.8	303	9	US-09-952-689-7	Sequence 7, Appl1
31	154.5	14.7	421	15	US-10-128-714-8570	Sequence 8570, Ap
32	144	13.7	499	15	US-10-128-714-3570	Sequence 3570, Ap
33	135	12.9	892	12	US-10-205-219-102	Sequence 102, App
34	131.5	12.5	1940	12	US-09-738-630-99	Sequence 99, Appl
35	109	10.4	24	12	US-09-942-024-90	Sequence 90, Appl
36	109	10.4	24	12	US-09-942-098-90	Sequence 90, Appl
37	108.5	10.4	1011	15	US-10-128-714-3079	Sequence 3079, Ap
38	108.5	10.4	1222	15	US-10-128-714-8079	Sequence 8079, Ap
39	107	10.2	30	12	US-09-942-024-39	Sequence 39, Appl
40	107	10.2	30	12	US-09-942-098-39	Sequence 39, Appl
41	106.5	10.2	685	12	US-10-259-165-320	Sequence 320, App
42	105.5	10.1	1119	15	US-10-128-714-3536	Sequence 3536, Ap
43	105	10.0	23	12	US-09-942-024-88	Sequence 88, Appl
44	105	10.0	23	12	US-09-942-098-88	Sequence 88, Appl
45	105	10.0	1576	15	US-10-037-182-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-09-942-024-2  
; Sequence 2, Application US/09942024  
; Publication No. US20030143650A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
; TITLE OF INVENTION: Serotype A/E Toxins  
; FILE REFERENCE: P-AR 4803  
; CURRENT APPLICATION NUMBER: US/09/942,024  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 206  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-942-024-2

Query Match 100.0%; Score 1048; DB 12; Length 206;  
Best Local Similarity 100.0%; Pred. No. 1.2e-90;  
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEDADMRNELEEMQRRADQADLESLESTRMLQLVESKDGAGIRTLVMDDEGEQJERI 60  
DB 1 MAEDADMRNELEEMQRRADQADLESLESTRMLQLVESKDGAGIRTLVMDDEGEQJERI 60  
QY EEGMDQINKDKKKEKNTLDGKFCGLVCPCNKLKSSDAYKKMGNNOGVVASOPARV 120  
DB 61 EEGMDQINKDKKKEKNTLDGKFCGLVCPCNKLKSSDAYKKMGNNOGVVASOPARV 120  
QY VDEREOMASGFTRRVYNDARENMENDEFOVSGIIGLNRHMLDNGNEIDTQNRQIDR 180  
DB 121 VDEREOMASGFTRRVYNDARENMENDEFOVSGIIGLNRHMLDNGNEIDTQNRQIDR 180  
QY 181 IMERADSNKTRIDEANQATKMLGSG 206

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 16, 2003, 19:21:26 ; Search time 5.09091 Seconds  
(without alignments)  
405.511 Million cell updates/sec

Title: US-09-942-098-1  
Perfect score: 39  
Sequence: 1 EANORATK 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPRMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirts:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	80	4 Q9BR45	Q9BR45 homo sapien
2	39	100.0	124	13 Q93578	Q93578 brachydanio
3	39	100.0	143	6 Q9GM34	Q9GM34 macaca fasc
4	39	100.0	203	13 Q93579	Q93579 brachydanio
5	39	100.0	206	4 Q96FM2	Q96FM2 homo sapien
6	34	87.2	162	16 Q8DF43	Q8DF43 vibrio vuln
7	32	82.1	212	5 Q8T354	Q8T354 loligo peal
8	31	79.5	241	12 Q8V219	Q8V219 human respi
9	31	79.5	241	12 Q09717	Q09717 human respi
10	31	79.5	241	12 Q09633	Q09633 human respi
11	31	79.5	241	12 Q04161	Q04161 human respi
12	31	79.5	241	12 Q8UYD5	Q8UYD5 human respi
13	31	79.5	241	12 Q8V218	Q8V218 human respi
14	31	79.5	241	12 P90196	P90196 human respi
15	31	79.5	244	5 Q9U408	Q9U408 echinococcu
16	31	79.5	244	5 Q24902	Q24902 echinococcu

17	31	79.5	1179	5 Q9BLR7	Q9BLR7 leishmania
18	31	79.5	2481	10 Q9FR53	Q9FR53 arabidopsis
19	31	79.5	2513	10 Q9LPM4	Q9LPM4 arabidopsis
20	30	76.9	83	2 Q85443	Q85443 pseudomonas
21	30	76.9	83	2 Q85440	Q85440 pseudomonas
22	30	76.9	83	2 Q85439	Q85439 pseudomonas
23	30	76.9	83	2 Q85431	Q85431 pseudomonas
24	30	76.9	125	4 Q8NBA4	Q8NBA4 homo sapien
25	30	76.9	125	4 Q99014	Q99014 prototheca
26	30	76.9	205	13 Q8AXM2	Q8AXM2 xenopus lae
27	30	76.9	206	13 Q8AXM1	Q8AXM1 xenopus lae
28	30	76.9	225	2 Q8RKE8	Q8RKE8 desulfohalobac
29	30	76.9	330	10 Q9F2N6	Q9F2N6 oryza sativ
30	30	76.9	346	13 Q90WN4	Q90WN4 xenopus lae
31	30	76.9	375	16 Q8FEG5	Q8FEG5 escherichia
32	30	76.9	445	16 Q8ZMD9	Q8ZMD9 salmonella
33	30	76.9	446	16 Q8Z443	Q8Z443 salmonella
34	30	76.9	609	3 Q9HFI2	Q9HFI2 neurospora
35	30	76.9	955	13 Q8JH11	Q8JH11 brachydanio
36	30	76.9	1206	5 Q9GYQ4	Q9GYQ4 caenorhabdi
37	30	76.9	1721	4 Q9P281	Q9P281 homo sapien
38	29	74.4	83	2 Q85432	Q85432 pseudomonas
39	29	74.4	89	16 Q99YZ6	Q99YZ6 streptococc
40	29	74.4	89	16 Q8P2H7	Q8P2H7 streptococc
41	29	74.4	94	16 Q8P1R5	Q8P1R5 streptococc
42	29	74.4	109	16 Q9KGL8	Q9KGL8 bacillus ha
43	29	74.4	148	16 Q97P37	Q97P37 streptococc
44	29	74.4	148	16 Q8DNN2	Q8DNN2 streptococc
45	29	74.4	175	8 Q8HTL5	Q8HTL5 chlamydomon

#### ALIGNMENTS

##### RESULT 1

Q9BR45 ID Q9BR45 PRELIMINARY; PRT; 80 AA.  
AC Q9BR45:  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE D11068F16.2.2 (Novel protein (Isoform 2)).  
GN SNAP25.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Babbage A.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL023913; CAC34535.1;  
DR InterPro; IPR000928; SNAP-25.  
DR InterPro; IPR000727; T\_SNARE.  
DR Pfam; PF00835; SNAP-25; 1.  
DR SMART; SM00397; T\_SNARE; 1.  
DR PROSITE; PSS0192; T\_SNARE; 1.  
SQ SEQUENCE 80 AA; 8993 MW; A120C6571AD9F071 CRC64;

Query Match Best Local Similarity 100.0%; Score 39; DB 4; Length 80;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EANORATK 8  
DB 68 EANORATK 75

RESULT 2  
ID Q93578 PRELIMINARY; PRT; 124 AA.  
AC Q93578:  
DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (Tremblrel. 08, last sequence update)  
 DE 01-OCT-2002 (Tremblrel. 22, last annotation update)  
 GN SNAP25A OR SNAP.  
 OS Brachydanio rerio (zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99057281; PubMed=9843147;  
 RA Ristinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,  
 RA Larhammer D.;  
 RT "Cloning of two loci for synapse protein Snap25 in zebrafish:  
 RT comparison of paralogous linkage groups suggests loss of one locus in  
 RT the mammalian lineage.";  
 RL J. Neurosci. Res. 54:563-573(1998).  
 DR EMBL: AF091593; AAC64289.1; -.  
 DR ZFIN: ZDB-GENE-980526-468; snap25a.  
 DR InterPro: IPR000928; SNAP-25.  
 DR InterPro: IPR000727; T\_SNARE.  
 DR Pfam: PF00835; SNAP-25; 1.  
 DR SMART: SM00397; T\_SNARE; 1.  
 DR PROSITE: PS50192; T\_SNARE; 1.  
 FT NON\_TER  
 SQ SEQUENCE 124 AA; 13616 MW; 50E27DBDB33D958C CRC64;

Query Match 100.0%; Score 39; DB 13; Length 124;  
 Best Local Similarity 100.0%; Pred. No. 0.48;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANORATK 8  
 DB 112 EANORATK 119

RESULT 3  
 Q9GM34 PRELIMINARY; PRT; 143 AA.  
 AC 09GM34;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)  
 DT 01-OCT-2002 (Tremblrel. 22, last annotation update)  
 DE Hypothetical 16.0 kDa protein.  
 OS Macaca fascicularis (Crap eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,  
 RA Suzuki Y., Sugano S., Hashimoto K.;  
 RT "Isolation of full-length cDNA clones from macaque brain cDNA  
 RT libraries.";  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB049852; BAB16738.1; -.  
 DR InterPro: IPR000928; SNAP-25.  
 DR InterPro: IPR000727; T\_SNARE.  
 DR Pfam: PF00835; SNAP-25; 1.  
 DR SMART: SM00397; T\_SNARE; 1.  
 DR PROSITE: PS50192; T\_SNARE; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 143 AA; 16043 MW; D625DBAAB0893FB0 CRC64;

Query Match 100.0%; Score 39; DB 6; Length 143;  
 Best Local Similarity 100.0%; Pred. No. 0.56;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANORATK 8  
 DB 111 EANORATK 119

DB 131 EANORATK 138  
 RESULT 4  
 ID 093579 PRELIMINARY; PRT; 203 AA.  
 AC 093579;  
 DT 01-NOV-1998 (Tremblrel. 08, Created)  
 DT 01-NOV-1998 (Tremblrel. 08, last sequence update)  
 DE SYNAPTOSOME-associated protein 25.2 (SYNAPTOSOME associated protein  
 DE 25.2)  
 GN SNAP25B OR SNAP.  
 OS Brachydanio rerio (zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ristinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,  
 RA Larhammer D.;  
 RT "Cloning of two loci for synapse protein Snap25 in zebrafish:  
 RT comparison of paralogous linkage groups suggests loss of one locus in  
 RT the mammalian lineage.";  
 RL J. Neurosci. Res. 0:0-0(1998).  
 DR EMBL: AF091594; AAC64290.1; -.  
 DR EMBL: AF091596; AAC73007.1; -.  
 DR ZFIN: ZDB-GENE-980526-392; snap25b.  
 DR InterPro: IPR000928; SNAP-25.  
 DR InterPro: IPR000727; T\_SNARE.  
 DR Pfam: PF00835; SNAP-25; 1.  
 DR SMART: SM00397; T\_SNARE; 2.  
 DR PROSITE: PS50192; T\_SNARE; 2.  
 SQ SEQUENCE 203 AA; 22647 MW; 93B759DDDC93F38 CRC64;

Query Match 100.0%; Score 39; DB 13; Length 203;  
 Best Local Similarity 100.0%; Pred. No. 0.8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANORATK 8  
 DB 191 EANORATK 198

RESULT 5  
 Q96FM2 PRELIMINARY; PRT; 206 AA.  
 AC 096FM2;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, last annotation update)  
 DE Similar to synaptosomal-associated protein, 25kD.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC010647; AAH10647.1; -.  
 DR InterPro: IPR000928; SNAP-25.  
 DR InterPro: IPR000727; T\_SNARE.  
 DR Pfam: PF00835; SNAP-25; 1.  
 DR SMART: SM00397; T\_SNARE; 2.  
 DR PROSITE: PS50192; T\_SNARE; 2.  
 SQ SEQUENCE 206 AA; 23336 MW; E272652C701EA984 CRC64;

Query Match 100.0%; Score 39; DB 4; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 0.82;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



OY 1 EANORATK 8  
 |||||  
 DB 194 EANORATK 201

## RESULT 6

Q8DF43 PRELIMINARY; PRT; 162 AA.  
 AC O8DF43;  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Hypothetical protein.  
 GN V10381.  
 OS *Vibrio vulnificus*.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; *Vibrio*.  
 OX NCBI\_TaxID=672;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CMCP6;  
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,  
 RA Choy, H.E.;  
 RT "Complete genome sequence of *Vibrio vulnificus* CMCP6."  
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE016798; AAC08905.1; -  
 KM Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 162 AA; 18029 MW; 65272C082012A474 CRC64;

Query Match 87.2%; Score 34; DB 16; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 8.6;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ANORATK 8  
 |||||  
 DB 124 ANORATK 130

RESULT 7  
 Q8T3S4 PRELIMINARY; PRT; 212 AA.  
 AC Q8T3S4;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE SNAP25 fusion protein.  
 OS *Loligo pealeii* (Longfin squid).  
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
 OC Decapodiformes; *Loliginidae*; *Loligo*.  
 OX NCBI\_TaxID=6621;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bracher A., Kadlec J., Betz H., Weissenhorn W.;  
 RT "X-ray structure of a neuronal complexin/SNARE complex from squid."  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Dresbach T., O'Connor V., Burns M., Augustine G., Betz H.;  
 RT "Squid SNAP25."  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF092757; AAM18191.1; -  
 DR InterPro: IPR000928; SNAP-25.  
 DR InterPro: IPR000727; T-SNARE.  
 DR Pfam: PF00835; SNAP-25; 1.  
 DR SMART: SM00397; t-SNARE; 2.  
 DR PROSITE: PS00192; T-SNARE; 2.  
 SQ SEQUENCE 212 AA; 23816 MW; 127601619DE79E2D CRC64;

Query Match 82.1%; Score 32; DB 5; Length 212;  
 Best Local Similarity 75.0%; Pred. No. 32;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EANORATK 8  
 |||||  
 DB 201 EANKRATK 208

## RESULT 8

Q8V219 PRELIMINARY; PRT; 241 AA.  
 AC Q8V219;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Phosphoprotein P.  
 OS Human respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; *Pneumovirinae*; *Pneumovirus*.  
 OX NCBI\_TaxID=11250;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-beijing;  
 RX MEDLINE=21364133; PubMed=11471029;  
 RA Zhao L.Q., Wang Z.L., Geng X.H., Qian Y., Deng J., Zhu R.N.,  
 RA Wang L.T., Liu C.Q., Chang R.X.;  
 RT "Sequence analysis of phosphoprotein genes of respiratory syncytial  
 RT virus field strains isolated in China."  
 RL Chung Hua Shih Yen Ho Lin Chuang Ping Tu Hsueh Tsa Chih  
 14:366-369(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-beijing;  
 RA Zhao L.Q., Wang Z.L., Geng X.H., Qian Y., Deng J., Zhu R.N.,  
 RA Wang L.T., Liu C.Q., Chang R.X.;  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF453422; AAI50987.1; -  
 DR InterPro: IPR003487; *Pneumo\_phosprot*.  
 DR Pfam: PF02478; *Pneumo\_phosprot*; 1.  
 SQ SEQUENCE 241 AA; 27246 MW; DFE092382BC2F073 CRC64;

Query Match 79.5%; Score 31; DB 12; Length 241;  
 Best Local Similarity 75.0%; Pred. No. 61;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EANORATK 8  
 |||||  
 DB 12 DANRATK 19

RESULT 9  
 Q09717 PRELIMINARY; PRT; 241 AA.  
 AC Q09717;  
 DT 01-JUL-1997 (TREMBLrel. 04, Created)  
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE Phosphoprotein (P).  
 GN P.  
 OS Respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; *Pneumovirinae*; *Pneumovirus*.  
 OX NCBI\_TaxID=12814;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-S2 ts1C;  
 RX MEDLINE=97185152; PubMed=9032893;  
 RA Tolley K.P., Marriott A.C., Simpson A., Plows D.J., Matthews D.A.,  
 RA Longhurst S.J., Evans J.E., Johnson J.L., Cane P.A., Easton A.J.,  
 RA Pringle C.R.;  
 RT "Identification of mutations contributing to the reduced virulence of  
 RT a modified strain of respiratory syncytial virus."  
 RL Vaccine 14:1637-1646(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-S2 ts1C;

Query Match 82.1%; Score 32; DB 5; Length 212;  
 Best Local Similarity 75.0%; Pred. No. 32;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RA Easton A.J.;  
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U39661; AAC57033.1; -;  
 DR InterPro: IPR003487; Pneumo\_phosprot.  
 DR Pfam: PF02478; Pneumo\_phosprot. 1.  
 SQ SEQUENCE 241 AA; 27134 MW; 3EED90A47955642C CRC64;

Query Match  
 Best Local Similarity 79.5%; Score 31; DB 12; Length 241;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EANORATK 8  
 DB 12 DANNRATK 19

RESULT 10  
 ID 009633 PRELIMINARY; PRT; 241 AA.  
 AC 009633;  
 DT 01-JUL-1997 (TREMBLrel. 04, Created)  
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE Phosphoprotein (P).  
 GN P.  
 OS Human respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OC NCBI\_TaxID=11250;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-S2;  
 RA MEDLINE=97185152; PubMed=9032893;  
 RA Tooley K.P., Marriott A.C., Simpson A., Plows D.J., Matthews D.A.,  
 RA Longhurst S.J., Evans J.E., Johnson J.L., Cane P.A., Easton A.J.,  
 RA Pringle C.R.;  
 RT "Identification of mutations contributing to the reduced virulence of  
 RT a modified strain of respiratory syncytial virus."  
 RL Vaccine 14:1637-1646(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-S2;  
 RA Easton A.J.;  
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U39662; AAC57023.1; -;  
 DR InterPro: IPR003487; Pneumo\_phosprot.  
 DR Pfam: PF02478; Pneumo\_phosprot. 1.  
 SQ SEQUENCE 241 AA; 27148 MW; 3EECC211478EAD42C CRC64;

Query Match  
 Best Local Similarity 79.5%; Score 31; DB 12; Length 241;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EANORATK 8  
 DB 12 DANNRATK 19

RESULT 11  
 ID 004161 PRELIMINARY; PRT; 241 AA.  
 AC 004161;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Phosphoprotein (Fragment).  
 GN P.  
 OS Human respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OC NCBI\_TaxID=11250;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-RSN-2;  
 RX MEDLINE=92197000; PubMed=1549911;  
 RA Caravokyri C., Pringle C.R.;  
 RT "Effect of changes in the nucleotide sequence of the P gene of  
 RT respiratory syncytial virus on the electrophoretic mobility of the P  
 RT protein."  
 RL Virus genes 6:53-62(1992).  
 DR EMBL: M67450; AAA47419.1; -;  
 DR InterPro: IPR002048; EF-hand.  
 DR InterPro: IPR003487; Pneumo\_phosprot.  
 DR Pfam: PF02478; Pneumo\_phosprot. 1.  
 DR PROSITE: PS00018; EF\_HAND; 1.  
 FT NON\_TER 241  
 SQ SEQUENCE 241 AA; 26977 MW; 8ED78553326AEB35 CRC64;

Query Match  
 Best Local Similarity 79.5%; Score 31; DB 12; Length 241;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EANORATK 8  
 DB 12 EANNRATK 19

RESULT 12  
 ID 080YD5 PRELIMINARY; PRT; 241 AA.  
 AC 080YD5;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Phosphoprotein P.  
 OS Human respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OC NCBI\_TaxID=11250;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-changchun, and guangzhou;  
 RX MEDLINE=21364133; PubMed=11471029;  
 RA Zhao L.Q., Wang Z.L., Geng X.H., Qian Y., Deng J., Zhu R.N.,  
 RA Wang L.T., Liu C.Q., Chang R.X.,  
 RA "Sequence analysis of phosphoprotein genes of respiratory syncytial  
 RT virus field strains isolated in China."  
 RL Chung Hua Shih Yen Ho Lin Chuang Ping Tu Hsueh Tsa Chih  
 RL 14:366-369(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-changchun, and guangzhou;  
 RA Zhao L.Q., Wang Z.L., Geng X.H., Qian Y., Deng J., Zhu R.N.,  
 RA Wang L.T., Liu C.Q., Chang R.X.,  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF453425; AAL50990.1; -;  
 DR EMBL: AF453423; AAL50988.1; -;  
 DR InterPro: IPR003487; Pneumo\_phosprot.  
 DR Pfam: PF02478; Pneumo\_phosprot. 1.  
 SQ SEQUENCE 241 AA; 27179 MW; 94404C0C6E06EF2 CRC64;

Query Match  
 Best Local Similarity 79.5%; Score 31; DB 12; Length 241;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EANORATK 8  
 DB 12 DANNRATK 19

RESULT 13  
 ID 08V218 PRELIMINARY; PRT; 241 AA.  
 AC 08V218;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Phosphoprotein P.  
 OS Human respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11250;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=hebei;  
 RX MEDLINE=21364133; PubMed=11471029;  
 RA Zhao L.Q., Wang Z.L., Geng X.H., Qian Y., Deng J., Zhu R.N.,  
 RA Wang L.T., Liu C.Q., Chang R.X.;  
 RT "Sequence analysis of phosphoprotein genes of respiratory syncytial  
 RT virus field strains isolated in China.";  
 RL Chung Hua Shih Yen Ho Lin Chuang Ping Tu Hsueh Tsa Chih  
 RL 14:366-369(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=hebei;  
 RA Zhao L.Q., Wang Z.L., Geng X.H., Qian Y., Deng J., Zhu R.N.,  
 RA Wang L.T., Liu C.Q., Chang R.X.;  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF53424; AAL50989.1; -;  
 DR InterPro: IPR003487; Pneumo\_phosprot. 1.  
 DR Pfam: PF02478; Pneumo\_phosprot. 1.  
 SQ SEQUENCE 241 AA; 27226 MW; 91613EBE9646899 CRC64;

Query Match 79.5%; Score 31; DB 12; Length 241;  
 Best Local Similarity 75.0%; Pred. No. 61;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EANORATK 8  
 Db 12 DANNRATK 19

RESULT 14  
 P90196 PRELIMINARY; PRT; 241 AA.  
 AC P90196;  
 DT 01-MAY-1997 (TREMblrel. 03, Created)  
 DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE Phosphoprotein.  
 GN P.  
 OS Human respiratory syncytial virus (strain A2).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.  
 OX NCBI\_TaxID=11259;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A2;  
 RX MEDLINE=97078805; PubMed=8918930;  
 RA Firestone C.Y., Whitehead S.S., Collins P.L., Murphy B.R.,  
 RA Crowe J.E. Jr.;  
 RT "Nucleotide sequence analysis of the respiratory syncytial virus  
 RT subgroup A cold-passaged (cp) temperature sensitive (ts) cpts-248/404  
 RT live attenuated virus vaccine candidate.";  
 RL Virology 225:419-422(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A2;  
 RX MEDLINE=97187925; PubMed=9035372;  
 RA Crowe J.E. Jr., Firestone C.Y., Whitehead S.S., Collins P.L.,  
 RA Murphy B.R.;  
 RT "Acquisition of the ts phenotype by a chemically mutagenized cold-  
 RT passed human respiratory syncytial virus vaccine candidate results  
 RT from the acquisition of a single mutation in the polymerase (L) gene.";  
 RL Virus Genes 13:269-273(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A2;  
 RA Whitehead S.S.;

RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A2;  
 RX MEDLINE=95266253; PubMed=7747420;  
 RA Connors M., Crowe J.E. Jr., Firestone C.Y., Murphy B.R., Collins P.L.;  
 RT "A cold-passaged, attenuated strain of human respiratory syncytial  
 RT virus contains mutations in the F and L genes.";  
 RL Virology 208:478-484(1995).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A2;  
 RX MEDLINE=98216821; PubMed=9557743;  
 RA Whitehead S.S., Junasz K., Firestone C.Y., Collins P.L., Murphy B.R.;  
 RT "Recombinant respiratory syncytial virus (RSV) bearing a set of  
 RT mutations from cold-passaged RSV is attenuated in chimpanzees.";  
 RL J. Virol. 72:4467-4471(1998).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A2;  
 RA Whitehead S.S., Collins P.L., Murphy B.R.;  
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U63644; AAC55965.1; -;  
 DR EMBL: U50363; AAB86671.1; -;  
 DR EMBL: U50362; AAB86659.1; -;  
 DR EMBL: AF035006; AAC14897.1; -;  
 DR InterPro: IPR003487; Pneumo\_phosprot.  
 DR Pfam: PF02478; Pneumo\_phosprot. 1.  
 SQ SEQUENCE 241 AA; 27134 MW; E2B15FFFA2DFC78E CRC64;

Query Match 79.5%; Score 31; DB 12; Length 241;  
 Best Local Similarity 75.0%; Pred. No. 61;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EANORATK 8  
 Db 12 DANNRATK 19

RESULT 15  
 Q90408 PRELIMINARY; PRT; 244 AA.  
 AC Q90408;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE 14-3-3 protein.  
 GN 14-3-3.  
 OS Echinococcus granulosus.  
 OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;  
 OC Cyclophyllidae; Taeniidae; Echinococcus.  
 OX NCBI\_TaxID=6210;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=sheep;  
 RX MEDLINE=21182697; PubMed=11289064;  
 RA Siles-Lucas M., Nunes C.P., Zaha A.;  
 RT "Comparative analysis of the 14-3-3 gene and its expression in  
 RT Echinococcus granulosus and Echinococcus multilocularis  
 RT metacystodes.";  
 RL Parasitology 122:281-287(2001).  
 DR HSP: AF207904; AAF19966.1; -;  
 DR HSP: P29312; 1A37  
 DR InterPro: IPR00308; 14-3-3.  
 DR Pfam: PF00244; 14-3-3; 1.  
 DR PRINTS: PR00305; 1433ZETA.  
 DR ProDom: PD000600; 14-3-3; 1.  
 DR SMART: SM00101; 14.3.3.1.  
 DR POSTRE: PS00797; 1433.2; 1.  
 SQ SEQUENCE 244 AA; 27430 MW; 1FBC36D3054937B CRC64;

Query Match 79.5%; Score 31; DB 5; Length 244;  
 Best Local Similarity 85.7%; Pred. No. 62;

Matches	6;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	EANORAT	7						
Db	155	EANOKAT	161						

Search completed: September 16, 2003, 19:29:39  
Job time : 7.09091 secs

## RESULT 13

G65060  
probable glucarate dehydratase (EC 4.2.1.40) - Escherichia coli (strain K-12)  
C:Species: Escherichia coli  
C>Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
C:Accession: G65060  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MIMD:97426617; PMID:9278503  
A:Accession: G65060  
A:Molecule type: DNA  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Residues: 1-446 <BLAT>  
A:Cross-references: GB:AE000362; GB:U00096; NID:g1789143; PIDN:AC75829.1; PID:g1789150;  
A:Experimental source: strain K-12, substrain MG1655  
C:Superfamily: glucarate dehydratase  
C:Keywords: carbon-oxygen lyase; hydro-lyase

## Query Match

76.9%; Score 30; DB 2; Length 446;  
Best local Similarity 75.0%; Pred. No. 57;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EANORATK 8

Db 373 EGNORLTK 380

## RESULT 14

G91084  
probable glucarate dehydratase [imported] - Escherichia coli (strain O157:H7, substrain  
C:Species: Escherichia coli  
C>Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Aug-2001  
C:Accession: G91084  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A:Reference number: A99629; MIMD:21156231; PMID:11258796  
A:Accession: G91084  
A:Molecule type: DNA  
A:Status: preliminary  
A:Residues: 1-446 <NAV>  
A:Cross-references: GB:BA000007; PIDN:BA37070.1; PID:g13363118; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain RIMD 0509952  
C:Genetics:  
A:Gene: ECS3647  
C:Superfamily: glucarate dehydratase

## Query Match

76.9%; Score 30; DB 2; Length 446;  
Best local Similarity 75.0%; Pred. No. 57;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EANORATK 8

Db 373 EGNORLTK 380

## RESULT 15

H85929  
probable glucarate dehydratase ygcX [imported] - Escherichia coli (strain O157:H7, subst  
C:Species: Escherichia coli  
C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C:Accession: H85929  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A:title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MIMD:21074935; PMID:11206551  
A:Accession: H85929  
A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-446 <STO>

A:Cross-references: GB:AE005174; NID:g12517262; PIDN:AG57900.1; GSPDB:GN00145; UMGF:

C:Experimental source: strain O157:H7, substrain EDD933

C:Genetics:

A:Gene: ygcX

C:Superfamily: glucarate dehydratase

## Query Match

76.9%; Score 30; DB 2; Length 446;  
Best local Similarity 75.0%; Pred. No. 57;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EANORATK 8

Db 373 EGNORLTK 380

Search completed: September 16, 2003, 19:30:46  
Job time : 3.07792 secs

A:Title: Nucleotide sequence of the fusion and phosphoprotein genes of human respiratory  
A:Reference number: S07428; MUID:88323192; PMID:3414184  
A:Accession: S07428  
A:Molecule type: mRNA  
A:Residues: 1-241 <LOP>  
A:Cross-references: EMBL:AL2644; NID:g333949; PIDN:AAA47415.1; PID:g333950  
C:Genetics:  
A:Gene: P  
C:Superfamily: respiratory syncytial virus phosphoprotein P  
C:Keywords: phosphoprotein

Query Match 79.5%; Score 31; DB 1; Length 241;  
Best Local Similarity 75.0%; Pred. No. 18;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EANDRATK 8  
DB 12 DANNRATK 19

RESULT 9  
T40577  
probable phosphatidylinositol 3-kinase - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_revision 15-Sep-2000 #text\_change 06-Oct-2000  
C:Accession: T39913; T40577  
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Oliver, K.; Harris, D.  
submitted to the EMBL Data Library, March 1999  
A:Reference number: Z21890  
A:Accession: T39913  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 365-2337 <LYN>  
A:Cross-references: EMBL:AL049558; PIDN:CAB40167.1; GSPDB:GN00067; SPDB:SPBC216.07C  
R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, January 1999  
A:Reference number: Z21938  
A:Accession: T40577  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-398 <SEE>  
A:Cross-references: EMBL:AL055216; PIDN:CAA22805.1; GSPDB:GN00067; SPDB:SPBC646.01C  
A:Experimental source: strain 972h-; cosmid c646  
C:Genetics:  
A:Gene: SPBC646.01C  
A:Map position: 2  
C:Superfamily: yeast TOR2 protein

Query Match 79.5%; Score 31; DB 2; Length 2337;  
Best Local Similarity 75.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EANDRATK 8  
DB 1120 EASORSTK 1127

RESULT 10  
G96536  
hypothetical protein F2J10.9 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: G96536  
R:Thellogidis, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewart, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: G96536  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-2513 <STO>  
A:Cross-references: GB:AE005173; NID:g8569097; PIDN:AAF76442.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: F2J10.9  
A:Map position: 1

Query Match 79.5%; Score 31; DB 2; Length 2513;  
Best Local Similarity 75.0%; Pred. No. 2e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EANDRATK 8  
DB 1215 EASORSTK 1222

RESULT 11  
T07210  
H+-transporting two-sector ATPase (EC 3.6.3.14) chain I - Chlorella vulgaris chloropi  
C:Species: Chlorella vulgaris  
C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 03-Jun-2002  
C:Accession: T07210  
R:Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Na  
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997  
A:Title: Complete nucleotide sequence of the chloroplast genome from the green alga C  
A:Reference number: Z15985; MUID:97303241; PMID:9155184  
A:Accession: T07210  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-175 <WAK>  
A:Cross-references: EMBL:AB001684; NID:g2224352; PIDN:BA57857.1; PID:g2224373  
C:Genetics:  
A:Gene: atcp  
A:Genome: chloroplast  
C:Superfamily: H+-transporting ATP synthase chain I  
C:Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; th

Query Match 76.9%; Score 30; DB 2; Length 175;  
Best Local Similarity 75.0%; Pred. No. 22;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EANDRATK 8  
DB 59 EADORATE 66

RESULT 12  
I50552  
synapse protein - marbled electric ray  
C:Species: Torpedo marmorata (marbled electric ray)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C:Accession: I50552  
R:Risinger, C.; Blomqvist, A.G.; Lundell, I.; Lambertsson, A.; Nassel, D.; Pieribone,  
J. Biol. Chem. 268, 24408-24414, 1993  
A:Title: Evolutionary conservation of synaptosome-associated protein 25 kDa (SNAP-25)  
A:Reference number: A49513; MUID:94043281; PMID:8226991  
A:Accession: I50552  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-210 <RIS>  
A:Cross-references: GB:L22020; NID:g431296; PIDN:AAA49284.1; PID:g431297

Query Match 76.9%; Score 30; DB 2; Length 210;  
Best Local Similarity 75.0%; Pred. No. 26;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EANDRATK 8  
DB 201 EANKRATK 208

```

RESULT 3
A37861
synaptosomal-associated 25k protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 21-Jul-2000
C:Accession: A37861
R:CatScis, S.; Iarhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991
A:Title: Expression of a conserved cell-type-specific protein in nerve terminals coincides
A:Reference number: A37861; MUID:91126080; PMID:1992470
A:Accession: A37861
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-206 <CAT>
A:Cross-references: GB:M57957; NID:g212673; PIDN:AAA49072.1; PID:g212674

Query Match
Best Local Similarity 100.0%; Score 39; DB 2; Length 206;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EANORATK 8
|||||
DB 194 EANORATK 201

RESULT 4
I53735
nerve terminal protein - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I53735
R:Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A:Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A:Reference number: I53735; MUID:94156217; PMID:8112622
A:Accession: I53735
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-206 <RES>
A:Cross-references: GB:LI9760; NID:g307425; PIDN:AA37545.1; PID:g307426
C:Genetics:
A:Gene: GDB:SNAP
A:Cross-references: GDB:355671; OMIM:600322
A:Map position: 20p11.2-20p11.2

Query Match
Best Local Similarity 100.0%; Score 39; DB 2; Length 206;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EANORATK 8
|||||
DB 194 EANORATK 201

RESULT 5
I67823
nerve terminal protein - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Nov-1999
C:Accession: I67823
R:Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A:Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A:Reference number: I53735; MUID:94156217; PMID:8112622
A:Accession: I67823
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-206 <RES>
A:Cross-references: GB:LI9761; NID:g307427; PIDN:AA37546.1; PID:g307428
C:Genetics:
A:Gene: GDB:SNAP

```

```

A:Cross-references: GDB:355671; OMIM:600322
A:Map position: 20p11.2-20p11.2

Query Match
Best Local Similarity 100.0%; Score 39; DB 2; Length 206;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EANORATK 8
|||||
DB 194 EANORATK 201

RESULT 6
A33623
synaptosomal-associated 25k protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 05-Nov-1999
C:Accession: A33623
R:Oyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billingsley, M.; Bloom, F.E.
J. Cell Biol. 109, 3039-3052, 1989
A:Title: The identification of a novel synaptosomal-associated protein, SNAP-25, diff
A:Reference number: A33623; MUID:90078337; PMID:2592413
A:Accession: A33623
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-206 <OYL>
A:Cross-references: GB:M22012; GB:X51673; NID:g200997; PIDN:AAA61741.1; PID:g200998

Query Match
Best Local Similarity 100.0%; Score 39; DB 2; Length 206;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EANORATK 8
|||||
DB 194 EANORATK 201

RESULT 7
RN2
phosphoprotein P - human respiratory syncytial virus (strain A2)
C:Species: human respiratory syncytial virus
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 16-Jul-1999
C:Accession: A04037
R:Satake, M.; Elango, N.; Venkatesan, S.
J. Virol. 52, 991-994, 1984
A:Title: Sequence analysis of the respiratory syncytial virus phosphoprotein gene.
A:Reference number: A04037; MUID:85033973; PMID:6548527
A:Accession: A04037
A:Molecule type: mRNA
A:Residues: 1-241 <SAT>
A:Cross-references: GB:M11486; GB:K02719; NID:g333925; PIDN:AA859853.1; PID:g333929
A:Genetics:
A:Gene: P
C:Superfamily: respiratory syncytial virus phosphoprotein P
C:Keywords: phosphoprotein

Query Match
Best Local Similarity 79.5%; Score 31; DB 1; Length 241;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EANORATK 8
|||||
DB 12 DANNRATK 19

RESULT 8
RN2PP
phosphoprotein P - human respiratory syncytial virus (strain Long)
C:Species: human respiratory syncytial virus
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: S07428
R:Lopez, J.A.; Villanueva, N.; Melero, J.A.; Portela, A.
Virus Res. 10, 249-262, 1988

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 16, 2003, 19:21:56 ; Search time 2.07792 Seconds  
(without alignments)  
370.249 Million cell updates/sec

Title: US-09-942-098-1

Perfect score: 39

Sequence: 1 EANORATK 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR\_76:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	100.0	203	2 I50481	synapse protein SN
2	39	100.0	204	2 I50480	synapse protein SN
3	39	100.0	205	2 A37861	synaptosomal-assoc
4	39	100.0	206	2 I53735	nerve terminal pro
5	39	100.0	206	2 I67823	synaptosomal-assoc
6	39	100.0	206	2 A33623	phosphoprotein P -
7	31	79.5	241	1 RRNZ	phosphoprotein P -
8	31	79.5	241	1 RRNZ	phosphoprotein P -
9	31	79.5	241	1 RRNZ	phosphoprotein P -
10	31	79.5	241	1 RRNZ	phosphoprotein P -
11	31	79.5	241	1 RRNZ	phosphoprotein P -
12	31	79.5	241	1 RRNZ	phosphoprotein P -
13	31	79.5	241	1 RRNZ	phosphoprotein P -
14	31	79.5	241	1 RRNZ	phosphoprotein P -
15	31	79.5	241	1 RRNZ	phosphoprotein P -
16	31	79.5	241	1 RRNZ	phosphoprotein P -
17	31	79.5	241	1 RRNZ	phosphoprotein P -
18	31	79.5	241	1 RRNZ	phosphoprotein P -
19	31	79.5	241	1 RRNZ	phosphoprotein P -
20	31	79.5	241	1 RRNZ	phosphoprotein P -
21	31	79.5	241	1 RRNZ	phosphoprotein P -
22	31	79.5	241	1 RRNZ	phosphoprotein P -
23	31	79.5	241	1 RRNZ	phosphoprotein P -
24	31	79.5	241	1 RRNZ	phosphoprotein P -
25	31	79.5	241	1 RRNZ	phosphoprotein P -
26	31	79.5	241	1 RRNZ	phosphoprotein P -
27	31	79.5	241	1 RRNZ	phosphoprotein P -
28	31	79.5	241	1 RRNZ	phosphoprotein P -
29	31	79.5	241	1 RRNZ	phosphoprotein P -

30	29	74.4	935	2 T50774	probable translati
31	29	74.4	1223	2 T17345	hypothetical prote
32	28	71.8	45	2 A83765	hypothetical prote
33	28	71.8	99	2 H97828	hypothetical prote
34	28	71.8	241	1 RRNZ	phosphoprotein P -
35	28	71.8	302	1 S07503	exodeoxyribonuclea
36	28	71.8	304	2 C90560	ABC transporter at
37	28	71.8	337	2 T48341	hypothetical prote
38	28	71.8	373	2 AB0604	probable oxidoredu
39	28	71.8	385	2 B6359	similar to seed ma
40	28	71.8	489	2 S35323	SOF1 protein - yea
41	28	71.8	491	2 S75449	hypothetical prote
42	28	71.8	596	2 B96834	hypothetical prote
43	28	71.8	637	2 B82175	conserved hypothet
44	28	71.8	1143	2 T22952	hypothetical prote
45	28	71.8	1251	2 JH0256	botulinum neurotox

#### ALIGNMENTS

##### RESULT 1

I50481 synapse protein SNAP-25 - goldfish

C:Species: Carassius auratus (goldfish)

C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000

C:Accession: I50481

R:Risinger, C.; Larhammer, D.

A:Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.

A:Reference number: A49632; MUID:94068448; PMID:8248151

A:Accession: I50481

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-203 <RIS>

A:Cross-references: GB:I22976; NID:g349430; PIDN:AAA16538.1; PID:g349431

C:Genetics:

A:Gene: SNAP-25

Query Match 100.0%; Score 39; DB 2; Length 203;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EANORATK 8

DB 191 EANORATK 198

##### RESULT 2

I50480 synapse protein SNAP-25 - goldfish

C:Species: Carassius auratus (goldfish)

C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000

C:Accession: I50480

R:Risinger, C.; Larhammer, D.

A:Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.

A:Reference number: A49632; MUID:94068448; PMID:8248151

A:Accession: I50480

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-204 <RIS>

A:Cross-references: GB:I22973; NID:g349426; PIDN:AAA16537.1; PID:g349427

C:Genetics:

A:Gene: SNAP-25

Query Match 100.0%; Score 39; DB 2; Length 204;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EANORATK 8

DB 192 EANORATK 199



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; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-942-024-44

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Query Match          100.0%; Score 39; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 EANQRATK 8
        |||||
Db      8 EANQRATK 15

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Search completed: September 16, 2003, 19:31:52  
 Job time : 2.07792 secs

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; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays for Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 16
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
; US-09-942-098-91
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Query Match          100.0%; Score 39; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
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```
Qy      1 EAMORATK 8
        |||||||
Db      6 EAMORATK 13
```

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RESULT 12
; US-09-942-098-94
; Sequence 94, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays for Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa-DABCYL modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 16
; OTHER INFORMATION: Xaa=EDANS modified glutamate
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
; US-09-942-098-94
```

```
Query Match          100.0%; Score 39; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      1 EAMORATK 8
        |||||||
Db      6 EAMORATK 13
```

```
RESULT 13
; US-09-942-024-30
; Sequence 30, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays for Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-942-024-30
```

```
Query Match          100.0%; Score 39; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      1 EAMORATK 8
        |||||||
Db      8 EAMORATK 15
```

```
RESULT 14
; US-09-942-024-31
; Sequence 31, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays for Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-942-024-31
```

```
Query Match          100.0%; Score 39; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      1 EAMORATK 8
        |||||||
Db      9 EAMORATK 16
```

```
RESULT 15
; US-09-942-024-44
; Sequence 44, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
```

RESULT 7  
US-09-942-024-29  
; Sequence 29, Application US/09942024  
; Publication No. US20030143650A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
; FILE REFERENCE: Serotype A/E Toxins  
; CURRENT APPLICATION NUMBER: US/09/942,024  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-942-024-29

Query Match  
Best Local Similarity 100.0%; Score 39; DB 12; Length 16;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANDRATK 8  
Db 8 EANDRATK 15

RESULT 8  
US-09-942-024-91  
; Sequence 91, Application US/09942024  
; Publication No. US20030143650A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
; FILE REFERENCE: Serotype A/E Toxins  
; CURRENT APPLICATION NUMBER: US/09/942,024  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 91  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
; NAME/KEY: MOD\_RES  
; LOCATION: 1  
; OTHER INFORMATION: Xaa-fluorescein-modified lysine  
; NAME/KEY: MOD\_RES  
; LOCATION: 16  
; OTHER INFORMATION: Xaa-tetramethylrhodamine-modified lysine  
; NAME/KEY: AMIDATION  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: at the C-terminal  
US-09-942-024-91

Query Match  
Best Local Similarity 100.0%; Score 39; DB 12; Length 16;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANDRATK 8  
Db 6 EANDRATK 13

RESULT 9  
US-09-942-024-94

; Sequence 94, Application US/09942024  
; Publication No. US20030143650A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
; FILE REFERENCE: Serotype A/E Toxins  
; CURRENT APPLICATION NUMBER: US/09/942,024  
; CURRENT FILING DATE: 2001-08-28  
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; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 94  
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; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
; NAME/KEY: MOD\_RES  
; LOCATION: 1  
; OTHER INFORMATION: Xaa-DABCYL modified lysine  
; NAME/KEY: MOD\_RES  
; LOCATION: 16  
; OTHER INFORMATION: Xaa-EDANS modified glutamate  
; NAME/KEY: AMIDATION  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: at the C-terminal  
US-09-942-024-94

Query Match  
Best Local Similarity 100.0%; Score 39; DB 12; Length 16;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANDRATK 8  
Db 6 EANDRATK 13

RESULT 10  
US-09-942-098-29  
; Sequence 29, Application US/09942098  
; Publication No. US20030143651A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Clostridial  
; FILE REFERENCE: P-AR 4802  
; CURRENT APPLICATION NUMBER: US/09/942,098  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-942-098-29

Query Match  
Best Local Similarity 100.0%; Score 39; DB 12; Length 16;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANDRATK 8  
Db 8 EANDRATK 15

RESULT 11  
US-09-942-098-91  
; Sequence 91, Application US/09942098  
; Publication No. US20030143651A1

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; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-942-098-1

Query Match
Best Local Similarity 100.0%; Score 39; DB 12; Length 8;
Pred. No. 5e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANORATK 8
Db 1 EANORATK 8

RESULT 3
US-09-942-024-27
; Sequence 27, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 13
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-942-024-27

Query Match
Best Local Similarity 100.0%; Score 39; DB 12; Length 13;
Pred. No. 0.053;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANORATK 8
Db 5 EANORATK 12

RESULT 4
US-09-942-098-27
; Sequence 27, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 13
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; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-942-098-27

Query Match
Best Local Similarity 100.0%; Score 39; DB 12; Length 13;
Pred. No. 0.053;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANORATK 8
Db 5 EANORATK 12

RESULT 5
US-09-942-024-28
; Sequence 28, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 15
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-942-024-28

Query Match
Best Local Similarity 100.0%; Score 39; DB 12; Length 15;
Pred. No. 0.061;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANORATK 8
Db 8 EANORATK 15

RESULT 6
US-09-942-098-28
; Sequence 28, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 15
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-942-098-28

Query Match
Best Local Similarity 100.0%; Score 39; DB 12; Length 15;
Pred. No. 0.061;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANORATK 8
Db 8 EANORATK 15
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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: September 16, 2003, 19:23:56 ; Search time 2.07792 Seconds  
(without alignments)  
573.239 Million cell updates/sec

Title: US-09-942-098-1  
Perfect score: 39  
Sequence: 1 EANORATK 8

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 556269 seqs, 148893369 residues

Total number of hits satisfying chosen parameters: 556269

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database : Published\_Applications\_AA:\*

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2: /cgn2_6/ptodata/2/pubppaa/PCR_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubppaa/PCR_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	8	12	US-09-942-024-1
2	39	100.0	8	12	US-09-942-098-1
3	39	100.0	13	12	US-09-942-024-27
4	39	100.0	13	12	US-09-942-098-27
5	39	100.0	15	12	US-09-942-024-28
6	39	100.0	15	12	US-09-942-098-28
7	39	100.0	16	12	US-09-942-024-29
8	39	100.0	16	12	US-09-942-098-29
9	39	100.0	16	12	US-09-942-024-91
10	39	100.0	16	12	US-09-942-098-91
11	39	100.0	16	12	US-09-942-024-30
12	39	100.0	17	12	US-09-942-098-30
13	39	100.0	17	12	US-09-942-024-31
14	39	100.0	17	12	US-09-942-098-31
15	39	100.0	17	12	US-09-942-024-44

16	39	100.0	17	12	US-09-942-024-45	Sequence 45, Appl
17	39	100.0	17	12	US-09-942-024-56	Sequence 56, Appl
18	39	100.0	17	12	US-09-942-098-30	Sequence 30, Appl
19	39	100.0	17	12	US-09-942-098-31	Sequence 31, Appl
20	39	100.0	17	12	US-09-942-098-44	Sequence 44, Appl
21	39	100.0	17	12	US-09-942-098-45	Sequence 45, Appl
22	39	100.0	17	12	US-09-942-098-56	Sequence 56, Appl
23	39	100.0	17	14	US-10-011-588-2	Sequence 2, Appl
24	39	100.0	18	12	US-09-942-024-32	Sequence 32, Appl
25	39	100.0	18	12	US-09-942-098-32	Sequence 32, Appl
26	39	100.0	19	12	US-09-942-024-85	Sequence 85, Appl
27	39	100.0	19	12	US-09-942-024-92	Sequence 92, Appl
28	39	100.0	19	12	US-09-942-024-95	Sequence 95, Appl
29	39	100.0	19	12	US-09-942-098-85	Sequence 85, Appl
30	39	100.0	19	12	US-09-942-098-92	Sequence 92, Appl
31	39	100.0	19	12	US-09-942-098-95	Sequence 95, Appl
32	39	100.0	21	12	US-09-942-024-89	Sequence 89, Appl
33	39	100.0	21	12	US-09-942-098-89	Sequence 89, Appl
34	39	100.0	22	12	US-09-942-024-93	Sequence 93, Appl
35	39	100.0	22	12	US-09-942-098-93	Sequence 93, Appl
36	39	100.0	23	12	US-09-942-024-88	Sequence 88, Appl
37	39	100.0	23	12	US-09-942-098-88	Sequence 88, Appl
38	39	100.0	24	12	US-09-942-024-90	Sequence 90, Appl
39	39	100.0	24	12	US-09-942-098-90	Sequence 90, Appl
40	39	100.0	33	12	US-09-942-024-33	Sequence 33, Appl
41	39	100.0	33	12	US-09-942-024-37	Sequence 37, Appl
42	39	100.0	33	12	US-09-942-024-38	Sequence 38, Appl
43	39	100.0	33	12	US-09-942-098-33	Sequence 33, Appl
44	39	100.0	33	12	US-09-942-098-37	Sequence 37, Appl
45	39	100.0	33	12	US-09-942-098-38	Sequence 38, Appl

## ALIGNMENTS

```
RESULT 1
US-09-942-024-1
: Sequence 1, Application US/09942024
: Publication No. US20030143650A1
: GENERAL INFORMATION:
: APPLICANT: Steward, Lance E.
: APPLICANT: Fernandez-Salas, Ester
: APPLICANT: Aoki, Kei Roger
: TITLE OF INVENTION: Fret Protease Assays For Botulinum
: TITLE OF INVENTION: Serotype A/E Toxins
: FILE REFERENCE: P-AR 4803
: CURRENT APPLICATION NUMBER: US/09/942,024
: CURRENT FILING DATE: 2001-08-28
: NUMBER OF SEQ ID NOS: 96
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: synthetic construct
US-09-942-024-1
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Query Match 100.0%; Score 39; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANORATK 8  
Db 1 EANORATK 8

RESULT 2  
US-09-942-098-1  
: Sequence 1, Application US/09942098  
: Publication No. US20030143651A1  
: GENERAL INFORMATION:  
: APPLICANT: Steward, Lance E.

XX Montal M;  
PI  
XX  
DR MPI; 1997-479986/44.  
XX

PT Excitation-secretory uncoupling peptide(s) for inhibiting  
PT neuro:transmitter release - used particularly for treating muscle  
PT spasticity, and for delivering drugs specifically to neural cells  
XX

PS Claim 1; Page 30; 61pp; English.  
XX

CC This sequence corresponds to residues 170-206 of the human 25 kD  
CC synaptosomal associated protein (SNAP-25), and is a inhibitory agent of  
CC the invention. The agents of the invention inhibit secretion of  
CC neurotransmitter from neuronal cells and is an excitation-secretory  
CC uncoupling peptide (I) of at least 20 amino acids (aa) all of which  
CC correspond substantially to any one of AA30097-W30102, or more  
CC generally any (I) that inhibits 50% of catecholamine secretion from  
CC bovine chromaffin cells at a concentration of 10 microm, especially 0.25  
CC microm, or less. (I) are used, as a replacement for Clostridium toxin, to  
CC inhibit release of neurotransmitters from synaptic vesicles, specifically  
CC for reducing muscle spasticity. Also (I) may be labelled to allow in  
CC vivo imaging of intracellular distribution of (I). Compounds for  
CC delivering the drug to neural cells provide targeted drug delivery, e.g.  
CC of substance P to brain tumours for induction of apoptosis. Unlike the  
CC neurotoxins, (I) are not toxic or immunogenic and are more readily  
CC available. Their therapeutic effect lasts for several days or weeks, so  
CC lower doses or less frequent treatments are required.  
XX

SQ Sequence 37 AA;

Query Match

100.0%; Score 39; DB 18; Length 37;

Best Local Similarity 100.0%; Pred.No. 0.27;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANORATK 8  
|||||||

DB 25 EANORATK 32

Search completed: September 16, 2003, 19:26:24  
Job time : 5.71429 secs

KM bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;  
 KM synaptosomal associated protein; SNAP-25.  
 OS Homo sapiens.  
 XX WO9734620-A1.  
 PM 25-SEP-1997.  
 PD 18-MAR-1997; 97WO-US04393.  
 XX 18-MAR-1996; 96US-0013599.  
 PR (REGC ) UNIV CALIFORNIA.  
 XX Montal M;  
 PI WPI, 1997-479986/44.  
 DR  
 XX  
 XX Excitation-secretory uncoupling peptide(s) for inhibiting  
 PT neuro:transmitter release - used particularly for treating muscle  
 PT spasticity, and for delivering drugs specifically to neural cells  
 PS Claim 14; Page 32; 61pp; English.  
 XX  
 XX This sequence corresponds to residues 187-206 of the human 25 kD  
 CC synaptosomal associated protein (SNAP-25), and is a inhibitory agent of  
 CC the invention. The agents of the invention inhibit secretion of  
 CC neurotransmitter from neuronal cells and is an excitation-secretory  
 CC uncoupling peptide (1) of at least 20 amino acids (aa) all of which  
 CC correspond substantially to any one of AAW30097-W30102, or more  
 CC generally any (1) that inhibits 50% of catecholamine secretion from  
 CC bovine chromaffin cells at a concentration of 10 microm, especially 0.25  
 CC microm, or less. (1) are used, as a replacement for Clostridium toxin, to  
 CC inhibit release of neurotransmitters from synaptic vesicles, specifically  
 CC for reducing muscle spasticity. Also (1) may be labelled to allow in  
 CC vivo imaging of intracellular distribution of (1). Compounds for  
 CC delivering the drug to neural cells provide targeted drug delivery, e.g.  
 CC of substance P to brain tumours for induction of apoptosis. Unlike the  
 CC neurotoxins, (1) are not toxic or immunogenic and are more readily  
 CC available. Their therapeutic effect lasts for several days or weeks, so  
 CC lower doses or less frequent treatments are required.  
 XX  
 XX Sequence 20 AA;  
 SQ  
 Query Match 100.0%; Score 39; DB 18; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 EANDRATK 8  
 |||||||  
 DB 8 EANDRATK 15  
 RESULT 14  
 AAW30099  
 ID AAW30099 standard; peptide; 26 AA.  
 XX  
 XX AAW30099;  
 AC  
 XX 06-APR-1998 (first entry)  
 DT  
 XX  
 XX Neurotransmitter secretion inhibitor #3.  
 DE  
 XX  
 XX Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;  
 KM excitation-secretory uncoupling peptide; catecholamine secretion;  
 KM bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;  
 KM synaptosomal associated protein; SNAP-25.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO9734620-A1.  
 PM  
 XX

PD 25-SEP-1997.  
 XX  
 XX 18-MAR-1997; 97WO-US04393.  
 PF  
 XX 18-MAR-1996; 96US-0013599.  
 PR  
 XX (REGC ) UNIV CALIFORNIA.  
 XX  
 XX Montal M;  
 PI WPI, 1997-479986/44.  
 DR  
 XX  
 XX Excitation-secretory uncoupling peptide(s) for inhibiting  
 PT neuro:transmitter release - used particularly for treating muscle  
 PT spasticity, and for delivering drugs specifically to neural cells  
 PS Claim 13; Page 31; 61pp; English.  
 XX  
 XX This sequence corresponds to residues 181-206 of the human 25 kD  
 CC synaptosomal associated protein (SNAP-25), and is a inhibitory agent of  
 CC the invention. The agents of the invention inhibit secretion of  
 CC neurotransmitter from neuronal cells and is an excitation-secretory  
 CC uncoupling peptide (1) of at least 20 amino acids (aa) all of which  
 CC correspond substantially to any one of AAW30097-W30102, or more  
 CC generally any (1) that inhibits 50% of catecholamine secretion from  
 CC bovine chromaffin cells at a concentration of 10 microm, especially 0.25  
 CC microm, or less. (1) are used, as a replacement for Clostridium toxin, to  
 CC inhibit release of neurotransmitters from synaptic vesicles, specifically  
 CC for reducing muscle spasticity. Also (1) may be labelled to allow in  
 CC vivo imaging of intracellular distribution of (1). Compounds for  
 CC delivering the drug to neural cells provide targeted drug delivery, e.g.  
 CC of substance P to brain tumours for induction of apoptosis. Unlike the  
 CC neurotoxins, (1) are not toxic or immunogenic and are more readily  
 CC available. Their therapeutic effect lasts for several days or weeks, so  
 CC lower doses or less frequent treatments are required.  
 XX  
 XX Sequence 26 AA;  
 SQ  
 Query Match 100.0%; Score 39; DB 18; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 0.18; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 EANDRATK 8  
 |||||||  
 DB 14 EANDRATK 21  
 RESULT 15  
 AAW30097  
 ID AAW30097 standard; peptide; 37 AA.  
 XX  
 XX AAW30097;  
 AC  
 XX 06-APR-1998 (first entry)  
 DT  
 XX  
 XX Neurotransmitter secretion inhibitor #1.  
 DE  
 XX  
 XX Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;  
 KM excitation-secretory uncoupling peptide; catecholamine secretion;  
 KM bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;  
 KM synaptosomal associated protein; SNAP-25.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO9734620-A1.  
 PM  
 XX 25-SEP-1997.  
 PD  
 XX 18-MAR-1997; 97WO-US04393.  
 PF  
 XX 18-MAR-1996; 96US-0013599.  
 PR  
 XX (REGC ) UNIV CALIFORNIA.  
 PA





XX Disclosure; Column 9: 28bp; English.  
 PS  
 CC The invention relates to an enzymatic assay for the quantitation of  
 CC type A botulinum toxin, by determining the proteolytic activity of  
 CC botulinum neurotoxin type A using fluorescamine detection. Botulinum  
 CC toxin A has been shown to cleave the synaptosomal neurotransmitter  
 CC peptide SNAP25 between residues 197-198. The method comprises adding  
 CC an analogue (e.g. AAY44022-Y44076) of the SNAP25 peptide (AAY44021,  
 CC amino acids 187-203 of human SNAP25) to a sample containing the  
 CC botulinum toxin A so that hydrolysis of the peptide is initiated, then  
 CC stopping hydrolysis of the peptide at different time points; and  
 CC measuring the amount of hydrolysis at each time point by combining with a  
 CC label capable of detecting free amino groups resulting from the  
 CC hydrolysis. The amount of botulinum toxin A present in the sample is  
 CC determined by comparing measurements with the amount of label produced  
 CC from a known concentration of toxin measured under similar conditions.  
 CC The method is useful for the quantitation of type A botulinum toxin.  
 CC  
 SQ Sequence 17 AA:  
 Query Match 100.0%; Score 39; DB 20; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EANORATK 8  
 |||||||  
 DB 8 EANORATK 15  
 RESULT 9  
 AAY44057  
 ID AAY44057 standard; peptide; 17 AA.  
 XX  
 AC AAY44057;  
 DT 18-JAN-2000 (first entry)  
 DE Human SNAP25 (amino acids 187-203) analogue #36.  
 XX  
 KW Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis;  
 KW fluorescamine; detection; human; synaptosomal protein; SNAP25;  
 KW hydrolysis; amino group.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN US5965699-A.  
 XX  
 PD 12-OCT-1999.  
 XX  
 PF 06-NOV-1996; 96US-0743894.  
 XX  
 PR 06-NOV-1996; 96US-0743894.  
 XX  
 PA (USSA ) US SEC OF ARMY.  
 PA  
 PI Bostian KA, Schmidt JJ;  
 PI  
 DR WPI: 1999-579939/49.  
 XX  
 PT Quantitation of type A botulinum toxin -  
 XX  
 PS Disclosure; Column 9: 28bp; English.  
 CC  
 CC The invention relates to an enzymatic assay for the quantitation of  
 CC type A botulinum toxin, by determining the proteolytic activity of  
 CC botulinum neurotoxin type A using fluorescamine detection. Botulinum  
 CC toxin A has been shown to cleave the synaptosomal neurotransmitter  
 CC peptide SNAP25 between residues 197-198. The method comprises adding  
 CC an analogue (e.g. AAY44022-Y44076) of the SNAP25 peptide (AAY44021,  
 CC amino acids 187-203 of human SNAP25) to a sample containing the  
 CC botulinum toxin A so that hydrolysis of the peptide is initiated, then

CC stopping hydrolysis of the peptide at different time points; and  
 CC measuring the amount of hydrolysis at each time point by combining with a  
 CC label capable of detecting free amino groups resulting from the  
 CC hydrolysis. The amount of botulinum toxin A present in the sample is  
 CC determined by comparing measurements with the amount of label produced  
 CC from a known concentration of toxin measured under similar conditions.  
 CC The method is useful for the quantitation of type A botulinum toxin.  
 CC  
 SQ Sequence 17 AA:  
 Query Match 100.0%; Score 39; DB 20; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EANORATK 8  
 |||||||  
 DB 8 EANORATK 15  
 RESULT 10  
 AAY44070  
 ID AAY44070 standard; peptide; 17 AA.  
 XX  
 AC AAY44070;  
 DT 18-JAN-2000 (first entry)  
 DE Human SNAP25 (amino acids 187-203) analogue D7N.  
 XX  
 KW Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis;  
 KW fluorescamine; detection; human; synaptosomal protein; SNAP25;  
 KW hydrolysis; amino group.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN US5965699-A.  
 XX  
 PD 12-OCT-1999.  
 XX  
 PF 06-NOV-1996; 96US-0743894.  
 XX  
 PR 06-NOV-1996; 96US-0743894.  
 XX  
 PA (USSA ) US SEC OF ARMY.  
 PA  
 PI Bostian KA, Schmidt JJ;  
 PI  
 DR WPI: 1999-579939/49.  
 XX  
 PT Quantitation of type A botulinum toxin -  
 XX  
 PS Disclosure; Column 15: 28bp; English.  
 CC  
 CC The invention relates to an enzymatic assay for the quantitation of  
 CC type A botulinum toxin, by determining the proteolytic activity of  
 CC botulinum neurotoxin type A using fluorescamine detection. Botulinum  
 CC toxin A has been shown to cleave the synaptosomal neurotransmitter  
 CC peptide SNAP25 between residues 197-198. The method comprises adding  
 CC an analogue (e.g. AAY44022-Y44076) of the SNAP25 peptide (AAY44021,  
 CC amino acids 187-203 of human SNAP25) to a sample containing the  
 CC botulinum toxin A so that hydrolysis of the peptide is initiated, then  
 CC stopping hydrolysis of the peptide at different time points; and  
 CC measuring the amount of hydrolysis at each time point by combining with a  
 CC label capable of detecting free amino groups resulting from the  
 CC hydrolysis. The amount of botulinum toxin A present in the sample is  
 CC determined by comparing measurements with the amount of label produced  
 CC from a known concentration of toxin measured under similar conditions.  
 CC The method is useful for the quantitation of type A botulinum toxin.  
 CC  
 SQ Sequence 17 AA:  
 Query Match 100.0%; Score 39; DB 20; Length 17;

[illegible]

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PE 06-NOV-1996; 96US-0743894.
XX
PR 06-NOV-1996; 96US-0743894.
XX
PA (USSA ) US SEC OF ARMY.
XX
PI Bostian KA, Schmidt JJ;
XX
DR WPI: 1999-579939/49.
XX
PT Quantitation of type A botulinum toxin -
XX
PS Disclosure; Column 9; 28pp; English.
XX
CC The invention relates to an enzymatic assay for the quantitation of
CC type A botulinum toxin, by determining the proteolytic activity of
CC botulinum neurotoxin type A using fluorescamine detection. Botulinum
CC toxin A has been shown to cleave the synaptosomal neurotransmitter
CC peptide SNAP25 between residues 197-198. The method comprises adding
CC an analogue (e.g. AAY44022-Y44076) of the SNAP25 peptide (AAY44021,
CC amino acids 187-203 of human SNAP25) to a sample containing the
CC botulinum toxin A so that hydrolysis of the peptide is initiated, then
CC stopping hydrolysis of the peptide at different time points; and
CC measuring the amount of hydrolysis at each time point by combining with a
CC label capable of detecting free amino groups resulting from the
CC hydrolysis. The amount of botulinum toxin A present in the sample is
CC determined by comparing measurements with the amount of label produced
CC from a known concentration of toxin measured under similar conditions.
CC The method is useful for the quantitation of type A botulinum toxin.
XX
SQ Sequence 17 AA:

Query Match 100.0%; Score 39; DB 20; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EANORATK 8
   |||||||
Db 8 EANORATK 15

RESULT 8
AAY44056
ID AAY44056 standard; peptide; 17 AA.
XX
AC AAY44056;
XX
DT 18-JAN-2000 (first entry)
XX
DE Human SNAP25 (amino acids 187-203) analogue #35.
XX
RW Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis;
RW fluorescamine; detection; human; synaptosomal protein; SNAP25;
RW hydrolysis; amino group.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US5965699-A.
XX
PD 12-OCT-1999.
XX
PF 06-NOV-1996; 96US-0743894.
XX
PR 06-NOV-1996; 96US-0743894.
XX
PA (USSA ) US SEC OF ARMY.
XX
PI Bostian KA, Schmidt JJ;
XX
DR WPI: 1999-579939/49.
XX
PT Quantitation of type A botulinum toxin -

```

OY 1 EAMORATK 8  
 XX |||||  
 DB 8 EAMORATK 15

## RESULT 4

AAV44021 standard; peptide; 17 AA.

AC AAV44021;

DT 18-JAN-2000 (first entry)

DE Amino acids 187-203 of human SNAP25.

KW Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis;  
 KW fluorescamine; detection; human; synaptosomal protein; SNAP25;  
 KW hydrolysis; amino group.

OS Homo sapiens.

PN US5965699-A.

PD 12-OCT-1999.

PF 06-NOV-1996; 96US-0743894.

PR 06-NOV-1996; 96US-0743894.

PA (USSA ) US SEC OF ARMY.

PI Bostian KA, Schmidt JJ;

DR WPI: 1999-579939/49.

PT Quantitation of type A botulinum toxin -

PS Claim 1; Column 4; 28pp; English.

XX The invention relates to an enzymatic assay for the quantitation of  
 CC type A botulinum toxin, by determining the proteolytic activity of  
 CC botulinum neurotoxin type A using fluorescamine detection. The method  
 CC comprises adding an analogue (e.g. AAV44022-Y44076) of this peptide  
 CC (which represents amino acids 187-203 of the human synaptosomal protein  
 CC SNAP25) to a sample containing the botulinum toxin A so that hydrolysis  
 CC of the peptide is initiated, then stopping hydrolysis of the peptide at  
 CC different time points, and measuring the amount of hydrolysis at each  
 CC time point by combining with a label capable of detecting free amino  
 CC groups resulting from the hydrolysis. The amount of botulinum toxin A  
 CC present in the sample is determined by comparing measurements with the  
 CC amount of label produced from a known concentration of toxin measured  
 CC under similar conditions. The method is useful for the quantitation of  
 CC type A botulinum toxin.

SQ Sequence 17 AA;

Query Match 100.0%; Score 39; DB 20; Length 17;

Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;

OY 1 EAMORATK 8  
 XX |||||  
 DB 8 EAMORATK 15

## RESULT 5

AAV44039 standard; peptide; 17 AA.

AC AAV44039;

DT 18-JAN-2000 (first entry)

XX Human SNAP25 (amino acids 187-203) analogue #18.  
 DE Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis;  
 KW fluorescamine; detection; human; synaptosomal protein; SNAP25;  
 KW hydrolysis; amino group.

OS Homo sapiens.  
 OS Synthetic.

FT key Location/Qualifiers  
 FT Modified-site 4 /label= Abu

PN US5965699-A.

PD 12-OCT-1999.

PF 06-NOV-1996; 96US-0743894.

PR 06-NOV-1996; 96US-0743894.

PA (USSA ) US SEC OF ARMY.

PI Bostian KA, Schmidt JJ;

DR WPI: 1999-579939/49.

PT Quantitation of type A botulinum toxin -

PS Disclosure; Column 7-8; 28pp; English.

XX The invention relates to an enzymatic assay for the quantitation of  
 CC type A botulinum toxin, by determining the proteolytic activity of  
 CC botulinum neurotoxin type A using fluorescamine detection. Botulinum  
 CC toxin A has been shown to cleave the synaptosomal neurotransmitter  
 CC peptide SNAP25 between residues 197-198. The method comprises adding  
 CC an analogue (e.g. AAV44022-Y44076) of the SNAP25 peptide (AAV44021,  
 CC amino acids 187-203 of human SNAP25) to a sample containing the  
 CC botulinum toxin A so that hydrolysis of the peptide is initiated, then  
 CC stopping hydrolysis of the peptide at different time points, and  
 CC measuring the amount of hydrolysis at each time point by combining with a  
 CC label capable of detecting free amino groups resulting from the  
 CC hydrolysis. The amount of botulinum toxin A present in the sample is  
 CC determined by comparing measurements with the amount of label produced  
 CC from a known concentration of toxin measured under similar conditions.  
 CC The method is useful for the quantitation of type A botulinum toxin.

SQ Sequence 17 AA;

Query Match 100.0%; Score 39; DB 20; Length 17;

Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0;

OY 1 EAMORATK 8  
 XX |||||  
 DB 8 EAMORATK 15

## RESULT 6

AAV44044 standard; peptide; 17 AA.

AC AAV44044;

DT 18-JAN-2000 (first entry)

DE Human SNAP25 (amino acids 187-203) analogue M16X.

KW Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis;  
 KW fluorescamine; detection; human; synaptosomal protein; SNAP25;  
 KW hydrolysis; amino group.



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 16, 2003, 19:11:00 ; Search time 5.71429 Seconds  
(without alignments)  
222.217 Million cell updates/sec

Title: US-09-942-098-1  
Perfect score: 39  
Sequence: 1 EAMQRAFK 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues  
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	12	20	AA44061 Human SNAP25 (amin
2	39	100.0	15	20	AA44058 Human SNAP25 (amin
3	39	100.0	16	20	AA44056 Human SNAP25 (amin
4	39	100.0	17	20	AA44021 Amino acids 187-20
5	39	100.0	17	20	AA44039 Human SNAP25 (amin
6	39	100.0	17	20	AA44044 Human SNAP25 (amin
7	39	100.0	17	20	AA44048 Human SNAP25 (amin
8	39	100.0	17	20	AA44056 Human SNAP25 (amin
9	39	100.0	17	20	AA44057 Human SNAP25 (amin

10	39	100.0	17	20	AA44070 Human SNAP25 (amin
11	39	100.0	17	23	ABG69065 Human polypeptide
12	39	100.0	19	22	AA815586 Human SNAP-25 N-te
13	39	100.0	20	18	AA30100 Neurotransmitter s
14	39	100.0	26	18	AA30099 Neurotransmitter s
15	39	100.0	37	18	AA30097 Neurotransmitter s
16	39	100.0	70	17	AA86823 SNAP-25 residues 1
17	39	100.0	86	22	AA815584 Human SNAP-25 N-te
18	39	100.0	116	23	AA015165 Clostridial neurot
19	39	100.0	206	18	AA30103 Synaptoosomal assoc
20	39	100.0	206	19	AA79198 Mouse SNAP-25 poly
21	39	100.0	206	19	AA43426 Mouse synaptoosomal
22	39	100.0	206	22	AA000246 Synaptoosomal-assoc
23	39	100.0	206	22	AA000252 SNARE homologue, s
24	39	100.0	206	22	AA000253 SNARE homologue, s
25	39	100.0	206	22	AA002638 Synaptoosomal-assoc
26	39	100.0	206	22	AA002640 Synaptoosomal-assoc
27	36	92.3	12	20	AA44037 Human SNAP25 (amin
28	36	92.3	13	20	AA44036 Human SNAP25 (amin
29	36	92.3	16	20	AA44027 Human SNAP25 (amin
30	36	92.3	16	20	AA44071 Human SNAP25 (amin
31	36	92.3	16	20	AA44072 Human SNAP25 (amin
32	36	92.3	16	20	AA44073 Human SNAP25 (amin
33	36	92.3	16	20	AA44074 Human SNAP25 (amin
34	36	92.3	17	20	AA44022 Human SNAP25 (amin
35	36	92.3	17	20	AA44024 Human SNAP25 (amin
36	36	92.3	17	20	AA44026 Human SNAP25 (amin
37	36	92.3	17	20	AA44038 Human SNAP25 (amin
38	36	92.3	17	20	AA44041 Human SNAP25 (amin
39	36	92.3	17	20	AA44043 Human SNAP25 (amin
40	36	92.3	17	20	AA44063 Human SNAP25 (amin
41	36	92.3	24	23	AA015162 Clostridial neurot
42	35	89.7	17	20	AA44047 Human SNAP25 (amin
43	35	89.7	17	20	AA44050 Human SNAP25 (amin
44	35	89.7	17	20	AA44052 Human SNAP25 (amin
45	35	89.7	17	20	AA44059 Human SNAP25 (amin

## ALIGNMENTS

RESULT 1	
AA44061	AA44061 standard; peptide: 12 AA.
ID	AA44061
XX	AA44061:
AC	18-JAN-2000 (first entry)
XX	
DT	Human SNAP25 (amino acids 187-203) analogue #40.
XX	
DE	
XX	
KW	Enzymatic assay; quantitation: type A botulinum neurotoxin; proteolysis;
KW	fluorescamine; detection: human; synaptoosomal protein; SNAP25;
KW	hydrolysis; amino group.
XX	
OS	Homo sapiens.
XX	
OS	Synthetic.
XX	
PN	US5965699-A.
XX	
PD	12-OCT-1999.
XX	
PF	06-NOV-1996; 96US-0743894.
XX	
PR	06-NOV-1996; 96US-0743894.
XX	
PA	(US5A ) US SEC OF ARMY.
XX	
PI	Bostian KA, Schmidt JF;
XX	
DR	WPI; 1999-579939/49.
XX	
PT	Quantitation of type A botulinum toxin -

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Db 181 IMEKADSNKTRIDEANAAATKMLGSG 206

Search completed: September 16, 2003, 19:26:26  
Job time : 149.143 secs



PT Treating a patient suffering from poisoning or at risk of poisoning by  
 PT a clostridial toxin, e.g. botulism, comprises administering a  
 PT toxin-resistant or toxin-inhibitory SNARE -

Example 1; Page - : 131pp; English.

XX The sequence represents the amino acid sequence of synaptosomal-  
 CC associated protein, SNAP25, mutant R198T/L203A, used in a new  
 CC method of treating a patient suffering from poisoning or at risk of  
 CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble  
 CC (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor)  
 CC to a cell of the patient, where the SNARE is resistant to proteolysis by  
 CC the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the  
 CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of  
 CC treating a patient in need of inhibition of SNARE-dependent exocytosis  
 CC from a cell capable of performing SNARE-dependent exocytosis, comprises  
 CC supplying a fragment, variant, fusion or derivative of a SNARE or an  
 CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin  
 CC inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is  
 CC useful in the manufacture of a medicament for the treatment of a patient  
 CC suffering from poisoning or at risk of poisoning by clostridial toxin,  
 CC e.g. from botulism or tetanus. The fragment, variant, fusion or  
 CC derivative of a SNARE or of an inhibitory SNARE, or a recombinant  
 CC polynucleotide encoding either of these SNARE polypeptides are useful in  
 CC the manufacture of medicament for the treatment of a patient in need of  
 CC inhibition of SNARE-dependent exocytosis. The method of treatment is  
 CC performing SNARE-dependent exocytosis. The method of treatment is  
 CC relatively fast, thus alleviating the symptoms when most severe and  
 CC taking the patient out of critical state.  
 CC Note: The present sequence is not shown in the specification but is  
 CC derived from the mouse SNAP-25 sequence given in figure 8 (see AAU00246).

XX Sequence 206 AA;

Query Match Best Local Similarity 99.0%; Score 1037; DB 22; Length 206;

Matches 204; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAEDADMRNLEEMORRAQLADESLESTRRMQLVEESKDAGIRLVMDEGEOLERI 60  
 Db 1 MAEDADMRNLEEMORRAQLADESLESTRRMQLVEESKDAGIRLVMDEGEOLERI 60  
 QY 61 EEEGMDQINKDKMKAENKLDLGFCCGVCPCPKLKSSDAKKKAMGNNODGVVAASOPARY 120  
 Db 61 EEEGMDQINKDKMKAENKLDLGFCCGVCPCPKLKSSDAKKKAMGNNODGVVAASOPARY 120  
 QY 121 VDREQMAISGFIIRVTNDARENEMDENLEQVSGIIGNLRHMAIDMGNEIDTQNRQIDR 180  
 Db 121 VDREQMAISGFIIRVTNDARENEMDENLEQVSGIIGNLRHMAIDMGNEIDTQNRQIDR 180  
 QY 181 IMEKADSNKTRIDEANORATKMLGSG 206  
 Db 181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 15

ID AAU00256 standard; Protein; 206 AA.

XX AAU00256;

XX 12-SEP-2001 (first entry)

DE Synaptosomal-associated protein, SNAP25, mutant Q197A/R198A.

XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;

KM toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;

KM synaptosomal-associated protein; mouse; mutant; mutein;

XX N-ethylmaleimide-sensitive fusion protein;

OS soluble NSF-attachment protein receptor.

XX Key Location/Qualifiers  
 FH Misc-difference 197  
 FT MISC-difference 198 /note= "Wild-type Gln substituted by Ala"  
 FT MISC-difference 198 /note= "Wild-type Arg substituted by Ala"  
 XX W0200118038-A2.  
 PN 15-MAR-2001.  
 PD 18-AUG-2000; 2000WO-GB03196.  
 XX 20-AUG-1999; 99US-0149993.  
 PR (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
 PA Dolly JO, O'Sullivan GA, Mohammed N, Foran PG;  
 PI WPI; 2001-226739/23.  
 DR  
 XX Treating a patient suffering from poisoning or at risk of poisoning by  
 PT a clostridial toxin, e.g. botulism, comprises administering a  
 PT toxin-resistant or toxin-inhibitory SNARE -  
 XX Example 1; Page - : 131pp; English.  
 XX The sequence represents the amino acid sequence of synaptosomal-  
 CC associated protein, SNAP25, mutant Q197A/R198A, used in a new  
 CC method of treating a patient suffering from poisoning or at risk of  
 CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble  
 CC (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor)  
 CC to a cell of the patient, where the SNARE is resistant to proteolysis by  
 CC the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the  
 CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of  
 CC treating a patient in need of inhibition of SNARE-dependent exocytosis  
 CC from a cell capable of performing SNARE-dependent exocytosis, comprises  
 CC supplying a fragment, variant, fusion or derivative of a SNARE or an  
 CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin  
 CC inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is  
 CC useful in the manufacture of a medicament for the treatment of a patient  
 CC suffering from poisoning or at risk of poisoning by clostridial toxin,  
 CC e.g. from botulism or tetanus. The fragment, variant, fusion or  
 CC derivative of a SNARE or of an inhibitory SNARE, or a recombinant  
 CC polynucleotide encoding either of these SNARE polypeptides are useful in  
 CC the manufacture of medicament for the treatment of a patient in need of  
 CC inhibition of SNARE-dependent exocytosis. The method of treatment is  
 CC performing SNARE-dependent exocytosis. The method of treatment is  
 CC relatively fast, thus alleviating the symptoms when most severe and  
 CC taking the patient out of critical state.  
 CC Note: The present sequence is not shown in the specification but is  
 CC derived from the mouse SNAP-25 sequence given in figure 8 (see AAU00246).

SO Sequence 206 AA;

Query Match Best Local Similarity 98.9%; Score 1036; DB 22; Length 206;

Matches 204; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAEDADMRNLEEMORRAQLADESLESTRRMQLVEESKDAGIRLVMDEGEOLERI 60  
 Db 1 MAEDADMRNLEEMORRAQLADESLESTRRMQLVEESKDAGIRLVMDEGEOLERI 60  
 QY 61 EEEGMDQINKDKMKAENKLDLGFCCGVCPCPKLKSSDAKKKAMGNNODGVVAASOPARY 120  
 Db 61 EEEGMDQINKDKMKAENKLDLGFCCGVCPCPKLKSSDAKKKAMGNNODGVVAASOPARY 120  
 QY 121 VDREQMAISGFIIRVTNDARENEMDENLEQVSGIIGNLRHMAIDMGNEIDTQNRQIDR 180  
 Db 121 VDREQMAISGFIIRVTNDARENEMDENLEQVSGIIGNLRHMAIDMGNEIDTQNRQIDR 180  
 QY 181 IMEKADSNKTRIDEANORATKMLGSG 206  
 Db 181 IMEKADSNKTRIDEANORATKMLGSG 206



PF 18-AUG-2000; 2000MO-GB03196.  
 XX  
 PR 20-AUG-1999; 99US-0149993.  
 XX  
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
 XX  
 PI Dolly JO, O'Sullivan GA, Mohammed N, Foran PG;  
 XX  
 DR WPI; 2001-226739/23.  
 XX  
 PT Treating a patient suffering from poisoning or at risk of poisoning by  
 PT a clostridial toxin, e.g. botulism, comprises administering a  
 PT toxin-resistant or toxin-inhibitory SNARE -  
 XX  
 PS Example 1; Page - : 131pp; English.  
 XX  
 CC The sequence represents the amino acid sequence of synaptosomal-  
 CC associated protein, SNAP25, mutant Q197K/R198K, used in a new  
 CC method of treating a patient suffering from poisoning or at risk of  
 CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble  
 CC (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor)  
 CC to a cell of the patient, where the SNARE is resistant to proteolysis by  
 CC the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the  
 CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of  
 CC treating a patient in need of inhibition of SNARE-dependent exocytosis  
 CC from a cell capable of performing SNARE-dependent exocytosis, comprises  
 CC supplying a fragment, variant, fusion or derivative of a SNARE or an  
 CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin  
 CC inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is  
 CC useful in the manufacture of a medicament for the treatment of a patient  
 CC suffering from poisoning or at risk of poisoning by clostridial toxin,  
 CC e.g. from botulism or tetanus. The fragment, variant, fusion or  
 CC derivative of a SNARE or of an inhibitory SNARE, or a recombinant  
 CC polynucleotide encoding either of these SNARE polypeptides are useful in  
 CC the manufacture of a medicament for the treatment of a patient in need of  
 CC inhibition of SNARE-dependent exocytosis from a cell capable of  
 CC performing SNARE-dependent exocytosis. The method of treatment is  
 CC relatively fast, thus alleviating the symptoms when most severe and  
 CC taking the patient out of critical state.  
 CC Note: The present sequence is not shown in the specification but is  
 CC derived from the mouse SNAP-25 sequence given in figure 8 (see AAU00246).  
 XX  
 SQ Sequence 206 AA;  
 Query Match 99.3%; Score 1041; DB 22; Length 206;  
 Best Local Similarity 99.0%; Pred. No. 3.5e-90;  
 Matches 204; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
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 DB 1 MAEDADMRELEEMORRADQDLADESLESTRRMQLQVEESKDGIRTLVWLDGEGQLERI 60  
 QY 61 EEGMDQINKDMKEAEKNTLDLGFGLCYCPCKLKSSDAYKAMGNNDDGVVAPSPARY 120  
 DB 61 EEGMDQINKDMKEAEKNTLDLGFGLCYCPCKLKSSDAYKAMGNNDDGVVAPSPARY 120  
 QY 121 VDREQMAISGFIIRVTNDARENEMDENLEQVSGIIGNLRHVALDMGNEIDTQNRQIDR 180  
 DB 121 VDREQMAISGFIIRVTNDARENEMDENLEQVSGIIGNLRHVALDMGNEIDTQNRQIDR 180  
 QY 181 IMEKADSNKTRIDEANQRATKMLGSG 206  
 DB 181 IMEKADSNKTRIDEANQRATKMLGSG 206  
 XX  
 RESULT 12  
 AAU00257  
 ID AAU00257 standard; Protein; 206 AA.  
 XX  
 AC AAU00257;  
 XX  
 DT 12-SEP-2001 (first entry)  
 XX

DE Synaptosomal-associated protein, SNAP25, mutant Q197A/R198K.  
 XX  
 XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;  
 KM toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;  
 KM synaptosomal-associated protein; mouse; mutant; mutein;  
 KM N-ethylmaleimide-sensitive fusion protein;  
 KM soluble NSF-attachment protein receptor.  
 XX  
 OS Mus sp.  
 OS Synthetic.  
 OS  
 FH Key Location/Qualifiers  
 FT Misc-difference 197  
 FT FT /note- "Wild-type Gln substituted by Ala"  
 FT FT /note- "Wild-type Arg substituted by Lys"  
 XX  
 PN MO200118038-A2.  
 XX  
 PD 15-MAR-2001.  
 XX  
 PF 18-AUG-2000; 2000MO-GB03196.  
 XX  
 PR 20-AUG-1999; 99US-0149993.  
 XX  
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
 XX  
 PI Dolly JO, O'Sullivan GA, Mohammed N, Foran PG;  
 XX  
 DR WPI; 2001-226739/23.  
 XX  
 PT Treating a patient suffering from poisoning or at risk of poisoning by  
 PT a clostridial toxin, e.g. botulism, comprises administering a  
 PT toxin-resistant or toxin-inhibitory SNARE -  
 XX  
 PS Example 1; Page - : 131pp; English.  
 XX  
 CC The sequence represents the amino acid sequence of synaptosomal-  
 CC associated protein, SNAP25, mutant Q197A/R198K, used in a new  
 CC method of treating a patient suffering from poisoning or at risk of  
 CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble  
 CC (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor)  
 CC to a cell of the patient, where the SNARE is resistant to proteolysis by  
 CC the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the  
 CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of  
 CC treating a patient in need of inhibition of SNARE-dependent exocytosis  
 CC from a cell capable of performing SNARE-dependent exocytosis, comprises  
 CC supplying a fragment, variant, fusion or derivative of a SNARE or an  
 CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin  
 CC inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is  
 CC useful in the manufacture of a medicament for the treatment of a patient  
 CC suffering from poisoning or at risk of poisoning by clostridial toxin,  
 CC e.g. from botulism or tetanus. The fragment, variant, fusion or  
 CC derivative of a SNARE or of an inhibitory SNARE, or a recombinant  
 CC polynucleotide encoding either of these SNARE polypeptides are useful in  
 CC the manufacture of a medicament for the treatment of a patient in need of  
 CC inhibition of SNARE-dependent exocytosis from a cell capable of  
 CC performing SNARE-dependent exocytosis. The method of treatment is  
 CC relatively fast, thus alleviating the symptoms when most severe and  
 CC taking the patient out of critical state.  
 CC Note: The present sequence is not shown in the specification but is  
 CC derived from the mouse SNAP-25 sequence given in figure 8 (see AAU00246).  
 XX  
 SQ Sequence 206 AA;  
 Query Match 99.1%; Score 1039; DB 22; Length 206;  
 Best Local Similarity 99.0%; Pred. No. 5.4e-90;  
 Matches 204; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MAEDADMRELEEMORRADQDLADESLESTRRMQLQVEESKDGIRTLVWLDGEGQLERI 60  
 DB 1 MAEDADMRELEEMORRADQDLADESLESTRRMQLQVEESKDGIRTLVWLDGEGQLERI 60

CC derived from the mouse SNAP-25 sequence given in figure 8 (see AAU00246).  
 XX Sequence 206 AA:  
 Query Match 99.4%; Score 1042; DB 22; Length 206;  
 Best Local Similarity 99.5%; Pred. No. 2.8e-90;  
 Matches 205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAEDADMNRELEEMORRDLADESLESTRRLQLVESKDGAGITVLMDQEGOLERI 60  
 DB 1 MAEDADMNRELEEMORRDLADESLESTRRLQLVESKDGAGITVLMDQEGOLERI 60  
 QY 61 EEGMDQINKDKMEAKENLTDLGKFCGLVCPCNKLKSSDAYKKANGNODGVVASQPARV 120  
 DB 61 EEGMDQINKDKMEAKENLTDLGKFCGLVCPCNKLKSSDAYKKANGNODGVVASQPARV 120  
 QY 121 VDREQMAISGCFIRRYTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTONRQIDR 180  
 DB 121 VDREQMAISGCFIRRYTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTONRQIDR 180  
 QY 181 IMEKADSNKTRIDEANORATKMLGSG 206  
 DB 181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 10  
 AAU02638  
 ID AAU02638 standard; Protein; 206 AA.  
 AC AAU02638;  
 DT 12-SEP-2001 (first entry)  
 DE Synaptosomal-associated protein, SNAP25, mutant M202A.  
 KM SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;  
 KM toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;  
 KM synaptosomal-associated protein; mouse; mutant; mutlein;  
 KM N-ethylmaleimide-sensitive fusion protein;  
 KM soluble NSF-attachment protein receptor.  
 OS Mus sp.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Misc-difference 202 /note= "Wild-type Met substituted by Ala"  
 FT  
 XX WO200118038-A2.  
 XX PD 15-MAR-2001.  
 XX PF 18-AUG-2000; 2000WO-GB03196.  
 XX PR 20-AUG-1999; 99US-0149993.  
 XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
 XX PI Dolly JO, O'Sullivan GA, Mohammed N, Foran PG;  
 XX WPI: 2001-226739/23.  
 XX DR  
 XX XX Treating a patient suffering from poisoning or at risk of poisoning by  
 PT a clostridial toxin, e.g. botulism, comprises administering a  
 PT toxin-resistant or toxin-inhibitory SNARE -  
 XX  
 PS Example 1; Page - ; 131pp; English.  
 CC The sequence represents the amino acid sequence of synaptosomal-  
 CC associated protein, SNAP25, mutant M202A, used in a new  
 CC method of treating a patient suffering from poisoning or at risk of  
 CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble  
 CC (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor)

CC to a cell of the patient, where the SNARE is resistant to proteolysis by  
 CC the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the  
 CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of  
 CC treating a patient in need of inhibition of SNARE-dependent exocytosis  
 CC from a cell capable of performing, SNARE-dependent exocytosis, comprises  
 CC supplying a fragment, variant, fusion or derivative of a SNARE or an  
 CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin  
 CC inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is  
 CC useful in the manufacture of a medicament for the treatment of a patient  
 CC suffering from poisoning or at risk of poisoning by clostridial toxin,  
 CC e.g. from botulism or tetanus. The fragment, variant, fusion or  
 CC derivative of a SNARE or of an inhibitory SNARE, or a recombinant  
 CC polynucleotide encoding either of these SNARE polypeptides are useful in  
 CC the manufacture of medicament for the treatment of a patient in need of  
 CC inhibition of SNARE-dependent exocytosis from a cell capable of  
 CC performing SNARE-dependent exocytosis. The method of treatment is  
 CC relatively fast, thus alleviating the symptoms when most severe and  
 CC taking the patient out of critical state.  
 CC Note: The present sequence is not shown in the specification but is  
 CC derived from the mouse SNAP-25 sequence given in figure 8 (see AAU00246).  
 XX  
 SQ Sequence 206 AA:  
 Query Match 99.4%; Score 1042; DB 22; Length 206;  
 Best Local Similarity 99.5%; Pred. No. 2.8e-90;  
 Matches 205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAEDADMNRELEEMORRDLADESLESTRRLQLVESKDGAGITVLMDQEGOLERI 60  
 DB 1 MAEDADMNRELEEMORRDLADESLESTRRLQLVESKDGAGITVLMDQEGOLERI 60  
 QY 61 EEGMDQINKDKMEAKENLTDLGKFCGLVCPCNKLKSSDAYKKANGNODGVVASQPARV 120  
 DB 61 EEGMDQINKDKMEAKENLTDLGKFCGLVCPCNKLKSSDAYKKANGNODGVVASQPARV 120  
 QY 121 VDREQMAISGCFIRRYTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTONRQIDR 180  
 DB 121 VDREQMAISGCFIRRYTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTONRQIDR 180  
 QY 181 IMEKADSNKTRIDEANORATKMLGSG 206  
 DB 181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 11  
 AAU00262  
 ID AAU00262 standard; Protein; 206 AA.  
 AC AAU00262;  
 DT 12-SEP-2001 (first entry)  
 DE Synaptosomal-associated protein, SNAP25, mutant Q197K/R198K.  
 KM SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;  
 KM toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;  
 KM synaptosomal-associated protein; mouse; mutant; mutlein;  
 KM N-ethylmaleimide-sensitive fusion protein;  
 KM soluble NSF-attachment protein receptor.  
 OS Mus sp.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Misc-difference 197 /note= "Wild-type Gln substituted by Lys"  
 FT Misc-difference 198 /note= "Wild-type Arg substituted by Lys"  
 FT  
 XX WO200118038-A2.  
 XX PD 15-MAR-2001.  
 XX

KW N-ethylmaleimide-sensitive fusion protein;  
 KW soluble NSF-attachment protein receptor.  
 XX  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 197 /note= "Wild-type Gln substituted by Ala"  
 XX  
 PN MO200118038-A2.  
 XX  
 PD 15-MAR-2001.  
 XX  
 PF 18-AUG-2000; 2000MO-GB03196.  
 XX  
 PR 20-AUG-1999; 99US-0149993.  
 XX  
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
 XX  
 PI Dolly JO, O'Sullivan GA, Mohammed N, Foran PG;  
 XX  
 DR WPI: 2001-226739/23.  
 XX  
 PT Treating a patient suffering from poisoning or at risk of poisoning by  
 FT a clostridial toxin, e.g. botulism, comprises administering a  
 PT toxin-resistant or toxin-inhibitory SNARE -  
 XX  
 PS Example 1; Page - ; 131pp; English.  
 XX  
 CC The sequence represents the amino acid sequence of synaptosomal-  
 CC associated protein, SNAP25, mutant Q197A, used in a new  
 CC method of treating a patient suffering from poisoning or at risk of  
 CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble  
 CC (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor)  
 CC to a cell of the patient, where the SNARE is resistant to proteolysis by  
 CC the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the  
 CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of  
 CC treating a patient in need of inhibition of SNARE-dependent exocytosis  
 CC from a cell capable of performing SNARE-dependent exocytosis, comprises  
 CC supplying a fragment, variant, fusion or derivative of a SNARE or an  
 CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin  
 CC inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is  
 CC useful in the manufacture of a medicament for the treatment of a patient  
 CC suffering from poisoning or at risk of poisoning by clostridial toxin,  
 CC e.g. from botulism or tetanus. The fragment, variant, fusion or  
 CC derivative of a SNARE or of an inhibitory SNARE, or a recombinant  
 CC polynucleotide encoding either of these SNARE polypeptides are useful in  
 CC the manufacture of medicament for the treatment of a patient in need of  
 CC inhibition of SNARE-dependent exocytosis from a cell capable of  
 CC performing SNARE-dependent exocytosis. The method of treatment is  
 CC relatively fast, thus alleviating the symptoms when most severe and  
 CC taking the patient out of critical state.  
 CC Note: The present sequence is not shown in the specification but is  
 CC derived from the mouse SNAP-25 sequence given in figure 8 (see AAU00246).  
 XX  
 SQ Sequence 206 AA:  
 Query Match 99.4%; Score 1042; DB 22; Length 206;  
 Best Local Similarity 99.5%; Pred. No. 2.8e-90;  
 Matches 205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 181 IMEKADSNKTRIDEANORATKMLGSG 206  
 |||||||  
 DB 181 IMEKADSNKTRIDEANARATKMLGSG 206  
 RESULT 9  
 AAU00261  
 ID AAU00261 standard; Protein; 206 AA.  
 XX  
 AC AAU00261;  
 XX  
 DT 12-SEP-2001 (first entry)  
 XX  
 DE Synaptosomal-associated protein, SNAP25, mutant R198A.  
 XX  
 KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;  
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;  
 KW synaptosomal-associated protein; mouse; mutant; mutein;  
 KW N-ethylmaleimide-sensitive fusion protein;  
 KW soluble NSF-attachment protein receptor.  
 XX  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 198 /note= "Wild-type Arg substituted by Ala"  
 FT  
 XX  
 PN WO200118038-A2.  
 XX  
 PD 15-MAR-2001.  
 XX  
 PF 18-AUG-2000; 2000MO-GB03196.  
 XX  
 PR 20-AUG-1999; 99US-0149993.  
 XX  
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
 XX  
 PI Dolly JO, O'Sullivan GA, Mohammed N, Foran PG;  
 XX  
 DR WPI: 2001-226739/23.  
 XX  
 PT Treating a patient suffering from poisoning or at risk of poisoning by  
 FT a clostridial toxin, e.g. botulism, comprises administering a  
 PT toxin-resistant or toxin-inhibitory SNARE -  
 XX  
 PS Example 1; Page - ; 131pp; English.  
 XX  
 CC The sequence represents the amino acid sequence of synaptosomal-  
 CC associated protein, SNAP25, mutant R198A used in a new  
 CC method of treating a patient suffering from poisoning or at risk of  
 CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble  
 CC (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor)  
 CC to a cell of the patient, where the SNARE is resistant to proteolysis by  
 CC the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the  
 CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of  
 CC treating a patient in need of inhibition of SNARE-dependent exocytosis  
 CC from a cell capable of performing SNARE-dependent exocytosis, comprises  
 CC supplying a fragment, variant, fusion or derivative of a SNARE or an  
 CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin  
 CC inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is  
 CC useful in the manufacture of a medicament for the treatment of a patient  
 CC suffering from poisoning or at risk of poisoning by clostridial toxin,  
 CC e.g. from botulism or tetanus. The fragment, variant, fusion or  
 CC derivative of a SNARE or of an inhibitory SNARE, or a recombinant  
 CC polynucleotide encoding either of these SNARE polypeptides are useful in  
 CC the manufacture of medicament for the treatment of a patient in need of  
 CC inhibition of SNARE-dependent exocytosis from a cell capable of  
 CC performing SNARE-dependent exocytosis. The method of treatment is  
 CC relatively fast, thus alleviating the symptoms when most severe and  
 CC taking the patient out of critical state.  
 CC Note: The present sequence is not shown in the specification but is

CC treating a patient in need of inhibition of SNARE-dependent exocytosis  
CC from a cell capable of performing SNARE-dependent exocytosis, comprises  
CC supplying a fragment, variant, fusion or derivative of a SNARE or an  
CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin  
CC inhibitory SNARE to a recombinant polynucleotide encoding the SNARE is  
CC useful in the manufacture of a medicament for the treatment of a patient  
CC suffering from poisoning or at risk of poisoning by clostridial toxin,  
CC e.g. from botulism or tetanus. The fragment, variant, fusion or  
CC derivative of a SNARE or of an inhibitory SNARE, or a recombinant  
CC polynucleotide encoding either of these SNARE polypeptides are useful in  
CC the manufacture of a medicament for the treatment of a patient in need of  
CC inhibition of SNARE-dependent exocytosis from a cell capable of  
CC performing SNARE-dependent exocytosis. The method of treatment is  
CC relatively fast, thus alleviating the symptoms when most severe and  
CC taking the patient out of critical state.  
CC Note: The present sequence is not shown in the specification but is  
CC derived from the mouse SNAP-25 sequence given in figure 8 (see AA000246).  
XX  
SQ Sequence 206 AA;  
Query Match 99.5%; Score 1043; DB 22; Length 206;  
Best Local Similarity 99.5%; Pred. No. 2.3e-90;  
Matches 205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MAEDADNRNLEEMQRRADQLADESLESTRMQLVVEESKDAGIRTLVLMDEGEQQLERI 60  
Db 1 MAEDADNRNLEEMQRRADQLADESLESTRMQLVVEESKDAGIRTLVLMDEGEQQLERI 60  
QY 61 EEGMDQINKDKMKEKELUTLDGKFCGLCYPCNKLKSSDAYKKWGNNGGVASQPARV 120  
Db 61 EEGMDQINKDKMKEKELUTLDGKFCGLCYPCNKLKSSDAYKKWGNNGGVASQPARV 120  
QY 121 VDREEQMAISGCFIRRYTNDARENEMDENLEOVSGIIGNLRHMAIDMGNEIDTQNRQIDR 180  
Db 121 VDREEQMAISGCFIRRYTNDARENEMDENLEOVSGIIGNLRHMAIDMGNEIDTQNRQIDR 180  
QY 181 IMEKADSNKTRIDEANORATKMLGSG 206  
Db 181 IMEKADSNKTRIDEANORATKMLGSG 206  
RESULT 7  
ID AA000259 standard; Protein: 206 AA.  
AC AA000259;  
DT 12-SEP-2001 (first entry)  
XX  
DE Synaptosomal-associated protein, SNAP25, mutant R198T.  
XX  
KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;  
KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;  
KW N-ethylmaleimide-sensitive fusion protein; mouse; mutant; mutain;  
KW soluble NSF-attachment protein receptor.  
XX  
OS Mus sp.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Msc-difference 198 /note= "Wild-type Arg substituted by Thr"  
XX  
XX  
PN WO200118038-A2.  
XX  
PD 15-MAR-2001.  
XX  
PF 18-AUG-2000; 2000WO-GB03196.  
XX  
PR 20-AUG-1999; 99US-0149993.  
XX  
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX  
PI Dolly JO, O'Sullivan GA, Mohammed N, Foran PG;  
XX  
DR WPI: 2001-226739/23.  
XX  
PT Treating a patient suffering from poisoning or at risk of poisoning by  
PT a clostridial toxin, e.g. botulism, comprises administering a  
PT toxin-resistant or toxin-inhibitory SNARE -  
XX  
XX  
PS Example 1: Page - : 131pp; English.  
XX  
CC The sequence represents the amino acid sequence of synaptosomal-  
CC associated protein, SNAP25, mutant R198T used in a new  
CC method of treating a patient suffering from poisoning or at risk of  
CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble  
CC (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor)  
CC to a cell of the patient, where the SNARE is resistant to proteolysis by  
CC the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the  
CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of  
CC treating a patient in need of inhibition of SNARE-dependent exocytosis  
CC from a cell capable of performing SNARE-dependent exocytosis, comprises  
CC supplying a fragment, variant, fusion or derivative of a SNARE or an  
CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin  
CC inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is  
CC useful in the manufacture of a medicament for the treatment of a patient  
CC suffering from poisoning or at risk of poisoning by clostridial toxin,  
CC e.g. from botulism or tetanus. The fragment, variant, fusion or  
CC derivative of a SNARE or of an inhibitory SNARE, or a recombinant  
CC polynucleotide encoding either of these SNARE polypeptides are useful in  
CC the manufacture of a medicament for the treatment of a patient in need of  
CC inhibition of SNARE-dependent exocytosis from a cell capable of  
CC performing SNARE-dependent exocytosis. The method of treatment is  
CC relatively fast, thus alleviating the symptoms when most severe and  
CC taking the patient out of critical state.  
CC Note: The present sequence is not shown in the specification but is  
CC derived from the mouse SNAP-25 sequence given in figure 8 (see AA000246).  
XX  
SQ Sequence 206 AA;  
Query Match 99.4%; Score 1042; DB 22; Length 206;  
Best Local Similarity 99.5%; Pred. No. 2.8e-90;  
Matches 205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MAEDADNRNLEEMQRRADQLADESLESTRMQLVVEESKDAGIRTLVLMDEGEQQLERI 60  
Db 1 MAEDADNRNLEEMQRRADQLADESLESTRMQLVVEESKDAGIRTLVLMDEGEQQLERI 60  
QY 61 EEGMDQINKDKMKEKELUTLDGKFCGLCYPCNKLKSSDAYKKWGNNGGVASQPARV 120  
Db 61 EEGMDQINKDKMKEKELUTLDGKFCGLCYPCNKLKSSDAYKKWGNNGGVASQPARV 120  
QY 121 VDREEQMAISGCFIRRYTNDARENEMDENLEOVSGIIGNLRHMAIDMGNEIDTQNRQIDR 180  
Db 121 VDREEQMAISGCFIRRYTNDARENEMDENLEOVSGIIGNLRHMAIDMGNEIDTQNRQIDR 180  
QY 181 IMEKADSNKTRIDEANORATKMLGSG 206  
Db 181 IMEKADSNKTRIDEANOTATKMLGSG 206  
RESULT 8  
ID AA000260 standard; Protein: 206 AA.  
AC AA000260;  
DT 12-SEP-2001 (first entry)  
XX  
XX  
DE Synaptosomal-associated protein, SNAP25, mutant Q197A.  
XX  
KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;  
KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;  
KW synaptosomal-associated protein; mouse; mutant; mutain;

QY 121 VDERQMAISGGFIRRVNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180  
 DB 121 VDERQMAISGGFIRRVNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180  
 QY 181 IMEKADSNKTRIDEANORATKMLGSG 206  
 DB 181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 5  
 AAU00253  
 ID AAU00253 standard; Protein; 206 AA.  
 XX AAU00253;  
 AC  
 XX  
 XX 12-SEP-2001 (first entry)  
 DT  
 XX  
 DE SNARE homologue, synaptosomal-associated protein, hSNAP25b.  
 XX  
 XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;  
 KM toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;  
 KW synaptosomal-associated protein; hSNAP25b; human.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200118038-A2.  
 PN  
 XX  
 XX 15-MAR-2001.  
 PD  
 XX  
 XX 18-AUG-2000; 2000WO-GB03196.  
 PF  
 XX  
 XX 20-AUG-1999; 99US-0149993.  
 PR  
 XX  
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
 PA  
 XX Dolly JO, O'Sullivan GA, Mohammed N, Foran PG;  
 PI  
 XX WPI; 2001-226739/23.  
 DR  
 XX N-PSDB; AAS00370.  
 DR  
 XX  
 PT Treating a patient suffering from poisoning or at risk of poisoning by  
 PT a clostridial toxin, e.g. botulism, comprises administering a  
 FT toxin-resistant or toxin-inhibitory SNARE -  
 XX  
 XX  
 PS Disclosure; Fig 8; 130pp; English.

The sequence represents the amino acid sequence of SNARE homologue, synaptosomal-associated membrane protein, hSNAP25b, used during analysis of SNAP-25. SNAP-25 mutants were used in a new method of treating a patient suffering from poisoning or at risk of poisoning by a clostridial toxin, comprising supplying a SNARE (soluble (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to a cell of the patient, where the SNARE is resistant to proteolysis by the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin (toxin-inhibitory SNARE). The protein can be used in a method of treating a patient in need of inhibiting of SNARE-dependent exocytosis from a cell capable of performing SNARE-dependent exocytosis, comprising supplying a fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE to the cell of the patient. The toxin resistant or toxin inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is useful in the manufacture of a medicament for the treatment of a patient suffering from poisoning or at risk of poisoning by clostridial toxin, e.g. from botulism or tetanus. The fragment, variant, fusion or derivative of a SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding either of these SNARE polypeptides are useful in the manufacture of a medicament for the treatment of a patient in need of inhibiting of SNARE-dependent exocytosis from a cell capable of performing SNARE-dependent exocytosis. The method of treatment is relatively fast, thus alleviating the symptoms when most severe and taking the patient out of critical state.

Sequence 206 AA:

Query Match 100.0%; Score 1048; DB 22; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-91;  
 Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEDADMNELEEMORRADOADESLESTRMLQLVESKDAGITLYMLDEQGLERI 60  
 DB 1 MAEDADMNELEEMORRADOADESLESTRMLQLVESKDAGITLYMLDEQGLERI 60  
 QY 61 BEGMDQIKKDKAEAKNLTIDGKFCGLVCPCNKTKSSDAYKKANGNODGVVASOPARV 120  
 DB 61 BEGMDQIKKDKAEAKNLTIDGKFCGLVCPCNKTKSSDAYKKANGNODGVVASOPARV 120  
 QY 121 VDERQMAISGGFIRRVNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180  
 DB 121 VDERQMAISGGFIRRVNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180  
 QY 181 IMEKADSNKTRIDEANORATKMLGSG 206  
 DB 181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 6  
 AAU02640  
 ID AAU02640 standard; Protein; 206 AA.  
 XX AAU02640;  
 AC  
 XX  
 XX 12-SEP-2001 (first entry)  
 DT  
 XX  
 DE Synaptosomal-associated protein, SNAP25, mutant L203A.  
 XX  
 XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;  
 KM toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;  
 KW synaptosomal-associated protein; mouse; mutant; mutelin;  
 KM N-ethylmaleimide-sensitive fusion protein;  
 XX soluble NSF-attachment protein receptor.  
 XX  
 OS Mus sp.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 203 /note="Wild-type leu substituted by Ala"  
 FT  
 XX  
 XX WO200118038-A2.  
 PN  
 XX  
 XX 15-MAR-2001.  
 PD  
 XX  
 XX 18-AUG-2000; 2000WO-GB03196.  
 PF  
 XX  
 XX 20-AUG-1999; 99US-0149993.  
 PR  
 XX  
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
 PA  
 XX Dolly JO, O'Sullivan GA, Mohammed N, Foran PG;  
 PI  
 XX WPI; 2001-226739/23.  
 DR  
 XX  
 PT Treating a patient suffering from poisoning or at risk of poisoning by  
 PT a clostridial toxin, e.g. botulism, comprises administering a  
 FT toxin-resistant or toxin-inhibitory SNARE -  
 XX  
 XX  
 PS Example 1; Page -; 131pp; English.

The sequence represents the amino acid sequence of synaptosomal-associated protein, SNAP25, mutant L203A, used in a new method of treating a patient suffering from poisoning or at risk of poisoning by a clostridial toxin, comprising supplying a SNARE (soluble (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to a cell of the patient, where the SNARE is resistant to proteolysis by the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin (toxin-inhibitory SNARE). The protein can be used in a method of

KW neurotransmitter; presynaptic membrane; central nervous system; tumour;  
 KW neurodegenerative disease; hormonal disorder; immunological disorder.  
 XX Mus sp.  
 XX US5693476-A.  
 PN 02-DEC-1997.  
 PD 24-FEB-1995; 95US-0393985.  
 PF 24-FEB-1995; 95US-0393985.  
 PR 24-FEB-1995; 95US-0393985.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 PI Scheller RH;  
 P1 WPI: 1998-031743/03.  
 DR N-PSDB; AAV01554.  
 XX  
 PT Screening assay for modulators of syntaxin binding - using peptide  
 PT comprising binding site of syntaxin, for identifying drugs useful  
 PT for treating CNS disorders, neuro-degenerative diseases, etc  
 XX  
 PS Disclosure: Column 67-72; 57pp; English.  
 XX  
 CC This amino acid sequence represents the mouse synaptosomal-associated  
 CC protein of 25 kD (SNAP-25). The invention relates to a method for  
 CC identifying a compound capable of affecting the binding of a  
 CC syntaxin-binding protein (SBP), e.g. SNAP-25, alpha-SNAP, n-secl or VAMP,  
 CC to syntaxin. The method comprises measuring the effect of the test  
 CC compound on the extent of binding between the SBP and the SBP-binding  
 CC site on syntaxin. The method can be used for identifying drugs capable  
 CC of inhibiting or stimulating neurotransmitter release at the active zones  
 CC of presynaptic membranes, which may be useful for treating CNS disorders,  
 CC affective or psychotic disorders, neurodegenerative diseases, hormonal or  
 CC immunological disorders or tumours.  
 CC  
 XX Sequence 206 AA;  
 SQ  
 Query Match 100.0%; Score 1048; DB 19; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-91;  
 Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAEDADMRNELEEMQRRADQLADESLESTRMLQLVEESKDAGIRTLVLMDEGEQLERI 60  
 DB 1 MAEDADMRNELEEMQRRADQLADESLESTRMLQLVEESKDAGIRTLVLMDEGEQLERI 60  
 QY 61 EEGMDQINKDKKEKKNLTDLGKFCGLVCPCNKLKSSDAYKKAMGNQDGVVASOPARV 120  
 DB 61 EEGMDQINKDKKEKKNLTDLGKFCGLVCPCNKLKSSDAYKKAMGNQDGVVASOPARV 120  
 QY 121 VDREQMAISGGFIRRYTNDARENMENLEQVSGIIGNLFHMLDMGNEIDTGNRQIDR 180  
 DB 121 VDREQMAISGGFIRRYTNDARENMENLEQVSGIIGNLFHMLDMGNEIDTGNRQIDR 180  
 QY 181 IMERKADSNKTRIDEANORATKMLGSG 206  
 DB 181 IMERKADSNKTRIDEANORATKMLGSG 206

RESULT 4  
 AAU00246  
 ID AAU00246 standard; Protein: 206 AA.  
 XX  
 AC AAU00246;  
 XX  
 DT 12-SEP-2001 (first entry)  
 XX  
 DE Synaptosomal-associated protein, SNAP25.  
 XX  
 KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;  
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;

KW synaptosomal-associated protein; mutagenic; PCR primer; mouse;  
 KW N-ethylmaleimide-sensitive fusion protein;  
 KW soluble NSF-attachment protein receptor.  
 XX Mus sp.  
 XX  
 XX Key Location/Qualifiers  
 FH Cleavage-site 180..181  
 FT /note="Peptide bond susceptible to cleavage by  
 FT clostridial neurotoxin"  
 FT Cleavage-site 197..198  
 FT /note="Peptide bonds susceptible to cleavage by  
 FT clostridial neurotoxin"  
 XX  
 XX WO200118038-A2.  
 XX  
 XX 15-MAR-2001.  
 XX  
 XX 18-AUG-2000; 2000WO-GB03196.  
 XX  
 XX 20-AUG-1999; 99US-0149993.  
 XX  
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
 PA Dolly JO, O'Sullivan GA, Mohammed N, Foran PG;  
 PI WPI: 2001-226739/23.  
 DR  
 XX  
 PT Treating a patient suffering from poisoning or at risk of poisoning by  
 PT a clostridial toxin, e.g. botulism, comprises administering a  
 PT toxin-resistant or toxin-inhibitory SNARE -  
 XX  
 XX Disclosure: Fig 8; 131pp; English.  
 PS  
 XX The sequence represents the amino acid sequence of synaptosomal-  
 CC associated protein, SNAP25. The sequence was used to  
 CC create SNAP-25 double/single point mutants and C-terminal deletion  
 CC mutants used in a new method of treating a patient suffering from  
 CC poisoning or at risk of poisoning by a clostridial toxin, comprising  
 CC supplying a SNARE (soluble (N-ethylmaleimide-sensitive fusion protein) -  
 CC attachment protein receptor) to a cell of the patient, where the SNARE is  
 CC resistant to proteolysis by the toxin (toxin-resistant SNARE) and/or is  
 CC capable of inhibiting the toxin (toxin-inhibitory SNARE). The protein can  
 CC be used in a method of treating a patient in need of inhibition of SNARE-  
 CC dependent exocytosis from a cell capable of performing SNARE-dependent  
 CC exocytosis, comprises supplying a fragment, variant, fusion or derivative  
 CC of a SNARE or an inhibitory SNARE to the cell of the patient. The toxin  
 CC resistant or toxin inhibitory SNARE or a recombinant polynucleotide  
 CC encoding the SNARE is useful in the manufacture of a medicament for the  
 CC treatment of a patient suffering from poisoning or at risk of poisoning  
 CC by clostridial toxin, e.g. from botulism or tetanus. The fragment,  
 CC variant, fusion or derivative of a SNARE or of an inhibitory SNARE, or a  
 CC recombinant polynucleotide encoding either of these SNARE polypeptides  
 CC are useful in the manufacture of medicament for the treatment of a  
 CC patient in need of inhibition of SNARE-dependent exocytosis from a cell  
 CC capable of performing SNARE-dependent exocytosis. The method of treatment  
 CC is relatively fast, thus alleviating the symptoms when most severe and  
 CC taking the patient out of critical state.  
 CC  
 XX Sequence 206 AA;  
 SQ  
 Query Match 100.0%; Score 1048; DB 22; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-91;  
 Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAEDADMRNELEEMQRRADQLADESLESTRMLQLVEESKDAGIRTLVLMDEGEQLERI 60  
 DB 1 MAEDADMRNELEEMQRRADQLADESLESTRMLQLVEESKDAGIRTLVLMDEGEQLERI 60  
 QY 61 EEGMDQINKDKKEKKNLTDLGKFCGLVCPCNKLKSSDAYKKAMGNQDGVVASOPARV 120  
 DB 61 EEGMDQINKDKKEKKNLTDLGKFCGLVCPCNKLKSSDAYKKAMGNQDGVVASOPARV 120



PT neuro:transmitter release - used particularly for treating muscle  
 PT spasticity, and for delivering drugs specifically to neural cells  
 XX  
 PS Disclosure; Page 27-28; 61pp; English.

CC This sequence represents the human 25 kD synaptosomal associated protein  
 CC (SNAP-25), which is an inhibitory agent of the invention. The agents of  
 CC the invention inhibit secretion of neurotransmitter from neuronal cells  
 CC and is an excitation-secretory uncoupling peptide (I) of at least 20  
 CC amino acids (aa) all of which correspond substantially to any one of  
 CC AAW30097-W30102, or more generally any (I) that inhibits 50% of  
 CC catecholamine secretion from bovine chromaffin cells at a concentration  
 CC of 10 microm, especially 0.25 microm, or less. (I) are used, as a  
 CC replacement for Clostridium toxin, to inhibit release of  
 CC neurotransmitters from synaptic vesicles, specifically for reducing  
 CC muscle spasticity. Also (I) may be labelled to allow in vivo imaging of  
 CC intracellular distribution of (I). Compounds for delivering the drug to  
 CC neural cells provide targeted drug delivery, e.g. of substance P to  
 CC brain tumours for induction of apoptosis. Unlike the neurotoxins, (I) are  
 CC not toxic or immunogenic and are more readily available. Their  
 CC therapeutic effect lasts for several days or weeks, so lower doses or  
 CC less frequent treatments are required.

XX Sequence 206 AA:

SQ  
 Query Match 100.0%; Score 1048; DB 18; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-91;  
 Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAEDADMNLEEMORRADQDLADESLESTRRLMLQVLESKDGIRTLVWLDQSGQLERI 60  
 DB 1 MAEDADMNLEEMORRADQDLADESLESTRRLMLQVLESKDGIRTLVWLDQSGQLERI 60  
 OY 61 EEGMDQINKDMKEAKENLTDLGKFCGLCYPCPNKTKSSDAYKKANGNODGVVASOPARV 120  
 DB 61 EEGMDQINKDMKEAKENLTDLGKFCGLCYPCPNKTKSSDAYKKANGNODGVVASOPARV 120  
 OY 121 VDERQOMASISGFIIRVTNDARENEMDENLEQVSGIIGLRHMLDMGNEIDTQNRQIDR 180  
 DB 121 VDERQOMASISGFIIRVTNDARENEMDENLEQVSGIIGLRHMLDMGNEIDTQNRQIDR 180  
 OY 181 IMEKADSNKTRIDEANORATKMLGSG 206  
 DB 181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 2  
 AAW79198  
 ID AAW79198 standard; Protein; 206 AA.

XX AAW79198;  
 XX  
 DT 25-NOV-1998 (first entry)  
 XX  
 DE Mouse SNAP-25 polypeptide.  
 XX  
 KW Hrs-2 polypeptide; ATP-preferring nucleotidase; SNAP-25; vesicle docking;  
 KW calcium-regulated secretion; secretory vesicle; secretory process; brain;  
 KW neurotransmitter release; presynaptic membrane; CNS disorder; depression;  
 KW Parkinson's disease; endocrine system; hormonal imbalance; cell division;  
 KW thought disorder; schizophrenia; degenerative disorder; anaesthesia; fat;  
 KW immune system; antigen processing; immunomodulator; viral processing;  
 KW central nervous system; vesicular release; affective disorder; human;  
 KW anti-tumour application; membrane trafficking regulation; mouse.

OS Mus sp.

XX W09838210-A2.

XX 03-SEP-1998.

XX 26-FEB-1998; 98WO-US03789.

PR 26-FEB-1997; 97US-0039159.

XX (STRD ) UNIV LELAND STANFORD JUNIOR.

XX Bean AJ, Schellier RH;

XX WPI; 1998-481140/41.

DR N-PSDB; AAW57558.

PT New isolated Hrs-2 nucleotidase - used in assays to identify  
 PT compounds capable of modulating calcium regulatory secretion of  
 PT secretory vesicles, such as in neurotransmitter release

PS Claim 16; Pages 42-44; 55pp; English.

CC This represents a mouse SNAP-25 polypeptide, a component of the protein  
 CC polypeptides thought to underlie vesicle docking and fusion. The  
 CC invention provides rat and human Hrs-2 polypeptides which are ATP-  
 CC preferring nucleotidase that associate with SNAP-25. For identifying a  
 CC compound capable of modulating calcium-regulated secretion of secretory  
 CC vesicles, a SNAP-25 polypeptide can be contacted with a Hrs-2  
 CC polypeptide, in the presence and absence of a test compound. The effect  
 CC of the test compound on the extent of binding between the SNAP-25 and  
 CC Hrs-2 polypeptides are measured and a compound is identified as effective  
 CC if its measured effect on the extent of binding is above a threshold  
 CC level. The products can be used for identifying drugs capable of  
 CC affecting secretory processes, such as neurotransmitter release at the  
 CC active zones of presynaptic membranes. Such drugs can be used for  
 CC treating disorders or conditions of the central nervous system by  
 CC selectively enhancing or inhibiting vesicular release in specific areas  
 CC of the brain, including affective disorders (e.g. depression), disorders  
 CC of thought (e.g. schizophrenia) and degenerative disorders (Parkinson's  
 CC disease), as well as applications such as anaesthesia. The drugs can  
 CC also be used therapeutically in other systems such as the endocrine  
 CC system for treatment of hormonal imbalances, the immune system for  
 CC intervention in antigen processing, secreted immunomodulators, and viral  
 CC processing, as well as anti-tumour applications, such as regulation of  
 CC membrane trafficking during rapid cell division.

SQ Sequence 206 AA:

Query Match 100.0%; Score 1048; DB 19; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-91;  
 Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAEDADMNLEEMORRADQDLADESLESTRRLMLQVLESKDGIRTLVWLDQSGQLERI 60  
 DB 1 MAEDADMNLEEMORRADQDLADESLESTRRLMLQVLESKDGIRTLVWLDQSGQLERI 60  
 OY 61 EEGMDQINKDMKEAKENLTDLGKFCGLCYPCPNKTKSSDAYKKANGNODGVVASOPARV 120  
 DB 61 EEGMDQINKDMKEAKENLTDLGKFCGLCYPCPNKTKSSDAYKKANGNODGVVASOPARV 120  
 OY 121 VDERQOMASISGFIIRVTNDARENEMDENLEQVSGIIGLRHMLDMGNEIDTQNRQIDR 180  
 DB 121 VDERQOMASISGFIIRVTNDARENEMDENLEQVSGIIGLRHMLDMGNEIDTQNRQIDR 180  
 OY 181 IMEKADSNKTRIDEANORATKMLGSG 206  
 DB 181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 3  
 AAW43426  
 ID AAW43426 standard; Protein; 206 AA.

XX AAW43426;

XX 27-APR-1998 (first entry)

XX Mouse synaptosomal-associated protein-25.

XX Binding domain; mouse; syntaxin; synaptosomal-associated protein; CNS;

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OM protein - protein search, using SW model

Run on: September 16, 2003, 19:11:00 ; Search time 147.143 Seconds

(without alignments)  
222.217 Million cell updates/sec

Title: US-09-942-098-2

Perfect score: 1048

Sequence: 1 MAEDADMRNELEEMQRRADQ.....SNKTRIDEANQATKMLGSG 206

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_19Jun03:\*

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2: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:\*

3: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:\*

4: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:\*

5: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:\*

6: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:\*

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18: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:\*

19: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:\*

20: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:\*

21: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:\*

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23: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*

24: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:\*

Pred.-No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1048	100.0	206	AAW30103	Synaptosomal assoc
2	1048	100.0	206	AAW79198	Mouse SNAP-25 poly
3	1048	100.0	206	AAW3426	Mouse synaptosomal
4	1048	100.0	206	AAU00246	Synaptosomal-assoc
5	1048	100.0	206	AAU00253	SNARE homologue, s
6	1043	99.5	206	AAU02640	Synaptosomal-assoc
7	1042	99.4	206	AAU00259	Synaptosomal-assoc
8	1042	99.4	206	AAU00260	Synaptosomal-assoc
9	1042	99.4	206	AAU00261	Synaptosomal-assoc

10	1042	99.4	206	AAU02638	Synaptosomal-assoc
11	1041	99.3	206	AAU00262	Synaptosomal-assoc
12	1039	99.1	206	AAU00257	Synaptosomal-assoc
13	1039	99.1	206	AAU00266	Synaptosomal-assoc
14	1037	99.0	206	AAU02171	Synaptosomal-assoc
15	1036	98.9	206	AAU00256	Synaptosomal-assoc
16	1036	98.9	206	AAU02639	Synaptosomal-assoc
17	1033	98.6	206	AAU00258	Synaptosomal-assoc
18	1026	97.9	203	AAU02636	Synaptosomal-assoc
19	1022	97.5	202	AAU00265	Synaptosomal-assoc
20	1017	97.0	201	AAU02637	Synaptosomal-assoc
21	1012	96.6	200	AAU00264	Synaptosomal-assoc
22	1009	96.3	198	AAU00255	Synaptosomal-assoc
23	1007	96.1	199	AAU00263	Synaptosomal-assoc
24	1004	95.8	206	AAU00252	SNARE homologue, s
25	625.5	59.7	212	ABR64447	Novel human diageno
26	613.5	58.5	211	ABG02947	SNARE homologue, s
27	613.5	58.5	211	AAU00251	Novel human diageno
28	609.5	58.2	213	AAU00251	Novel human diageno
29	587	56.0	213	AAU00251	Novel human diageno
30	581	55.4	116	AAO15165	Human prostate can
31	512	48.9	175	ABJ19402	Clostridial neurot
32	451	43.0	106	AAU03825	Human intracellular
33	451	43.0	106	AAU03825	Human secreted pro
34	403	38.5	86	AAU03826	Human secreted pro
35	391.5	37.4	86	AAU03826	Human secreted pro
36	361.5	34.5	129	AAU03705	Human SNAP-25 N-te
37	353	33.7	70	AAU03705	Human SNAP-25 N-te
38	310	29.6	64	AAU00764	Human colon cancer
39	253	24.1	513	AAU02996	SNAP-25 residues 1
40	253	24.1	546	AAU02995	Human secreted pro
41	253	24.1	714	AAU02994	Human secreted pro
42	244	23.3	49	AAU0386	Human brain expres
43	230	21.9	247	AAU09027	Arabidopsis thalia
44	230	21.9	247	AAU03785	Arabidopsis thalia
45	230	21.9	247	AAU03785	Arabidopsis thalia

#### ALIGNMENTS

RESULT 1	
AAW30103	AAW30103 standard; peptide: 206 AA.
AC	
XX	AAW30103;
DT	06-APR-1998 (first entry)
XX	
DE	Synaptosomal associated protein.
XX	
KW	Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;
KW	excitation-secretory uncoupling peptide; catecholamine secretion;
KW	bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;
KW	synaptosomal associated protein; SNAP-25.
XX	
OS	Homo sapiens.
XX	
PN	W09734620-A1.
XX	
PD	25-SEP-1997.
XX	
PF	18-MAR-1997; 97WO-US04393.
XX	
PR	18-MAR-1996; 96US-0013599.
XX	
PA	(RBCG ) UNIV CALIFORNIA.
XX	
PI	Montal M;
XX	
DR	WPI; 1997-479986/44.
XX	
PT	Excitation-secretory uncoupling peptide(s) for inhibiting

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## OM protein - protein search, using sw model

Run on: September 16, 2003, 19:21:56 ; Search time 4.41558 Seconds  
(without alignments)  
370.249 Million cell updates/sec

Title: US-09-942-098-2\_COPY\_187\_203  
Perfect score: 83  
Sequence: 1 SNKTRIDEANORATKML 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	203	2 I50481	synapse protein SN
2	83	100.0	204	2 I50480	synapse protein SN
3	83	100.0	206	2 A37861	synaptosomal-assoc
4	83	100.0	206	2 I53735	nerve terminal pro
5	83	100.0	206	2 I67823	synaptosomal-assoc
6	83	100.0	206	2 A33623	synapse protein -
7	65	78.3	210	2 I50552	SNARE protein 23 -
8	50	60.2	210	2 JCS512	vesicle-membrane f
9	46	55.4	158	2 JCS297	hypothetical prote
10	46	55.4	211	2 JCS296	hypothetical prote
11	44	53.0	228	2 T26553	outer membrane lip
12	44	53.0	234	2 T26553	transmembrane tran
13	42	50.6	83	2 A33854	hypothetical prote
14	42	50.6	401	2 B81436	hypothetical prote
15	42	50.6	420	2 S50562	hypothetical prote
16	41	49.4	393	2 T33127	pre-mRNA splicing
17	41	49.4	494	2 S64386	lipoprotein (impor
18	41	49.4	642	2 G90551	hypothetical prote
19	40	48.2	540	2 T34187	methy1-accepting c
20	40	48.2	575	2 F66966	matng type silenc
21	39	47.6	1314	2 T08481	hypothetical prote
22	39	47.0	243	2 T20653	outer membrane pro
23	39	47.0	680	2 H70347	protein F59B2.12 l
24	38.5	46.4	918	2 G88545	hypothetical prote
25	38.5	46.4	943	2 S31132	hypothetical prote
26	38	45.8	142	2 T48816	hypothetical prote
27	38	45.8	151	2 G95369	SyB2 transcriptio
28	38	45.8	176	2 D72668	hypothetical prote
29	38	45.8	181	2 JC4946	ADP-ribosylation f

30	38	45.8	181	2 A45422	ADP-ribosylation f
31	38	45.8	217	2 A47483	cysteine-rich omeg
32	38	45.8	219	2 A81996	hypothetical prote
33	38	45.8	294	2 S68784	cathepsin L - Para
34	38	45.8	317	2 A72295	conserved hypothet
35	38	45.8	414	2 T26205	hypothetical prote
36	38	45.8	465	2 T16618	hypothetical prote
37	38	45.8	586	1 C64988	probable sulfatase
38	38	45.8	586	2 H91013	probable sulfatase
39	38	45.8	586	2 B85858	probable sulfatase
40	38	45.8	643	2 T32269	hypothetical prote
41	38	45.8	869	2 H89864	hypothetical prote
42	38	45.8	1272	2 C96637	hypothetical prote
43	38	45.8	1578	2 S76238	hypothetical prote
44	37	44.6	150	2 T19447	hypothetical prote
45	37	44.6	227	2 D83271	probable ATP-blnd1

## ALIGNMENTS

## RESULT 1

I50481  
synapse protein SNAP-25 - goldfish  
C:Species: Carassius auratus (goldfish)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C:Accession: I50481  
R:Risinger, C.; Larhammar, D.  
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993  
A:Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.  
A:Reference number: A49632; MUID:94068448; PMID:8248151  
A:Accession: I50481  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-203 <RIS>  
A:Cross-references: GB:L22976; NID:g349430; PIDN:AAA16538.1; PTD:g349431  
A:Genetics:  
A:Gene: SNAP-25

Query Match 100.0%; Score 83; DB 2; Length 203;  
Best Local Similarity 100.0%; Pred. No. 6; Be-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SNKTRIDEANORATKML 17  
|||||  
DB 184 SNKTRIDEANORATKML 200

## RESULT 2

I50480  
synapse protein SNAP-25 - goldfish  
C:Species: Carassius auratus (goldfish)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C:Accession: I50480  
R:Risinger, C.; Larhammar, D.  
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993  
A:Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.  
A:Reference number: A49632; MUID:94068448; PMID:8248151  
A:Accession: I50480  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-204 <RIS>  
A:Cross-references: GB:L22973; NID:g349426; PIDN:AAA16537.1; PTD:g349427  
A:Genetics:  
A:Gene: SNAP-25

Query Match 100.0%; Score 83; DB 2; Length 204;  
Best Local Similarity 100.0%; Pred. No. 6; Be-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SNKTRIDEANORATKML 17  
|||||  
DB 185 SNKTRIDEANORATKML 201

```

RESULT 3
A37861
synaptosomal-associated 25K protein - chicken
C:Species: Gallus gallus (chicken)
C>Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 21-Jul-2000
C:Accession: A37861
R:CatScias, S.; Larhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991
A:Title: Expression of a conserved cell-type-specific protein in nerve terminals coincides
A:Reference number: A37861; MUID:91126080; PMID:1992470
A:Accession: A37861
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-206 <CAT>
A:Cross-references: GB:M57957; NID:g212673; PIDN:AAA49072.1; PID:g212674

Query Match
Best Local Similarity 100.0%; Score 83; DB 2; Length 206;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKML 17
187 SNKTRIDEANORATKML 203

RESULT 4
I53735
nerve terminal protein - human
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I53735
R:Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A:Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A:Reference number: I53735; MUID:94156217; PMID:8112622
A:Accession: I53735
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-206 <RES>
A:Cross-references: GB:LI9760; NID:g307425; PIDN:AAC37545.1; PID:g307426
C:Genetics:
A:Gene: GDB:SNAP
A:Cross-references: GDB:355671; OMIM:600322
A:Map position: 20p11.2-20p11.2

Query Match
Best Local Similarity 100.0%; Score 83; DB 2; Length 206;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKML 17
187 SNKTRIDEANORATKML 203

RESULT 5
I67823
nerve terminal protein - human
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Nov-1999
C:Accession: I67823
R:Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A:Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A:Reference number: I53735; MUID:94156217; PMID:8112622
A:Accession: I67823
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-206 <RES>
A:Cross-references: GB:LI9761; NID:g307427; PIDN:AAC37546.1; PID:g307428
C:Genetics:
A:Gene: GDB:SNAP

```

```

A:Cross-references: GDB:355671; OMIM:600322
A:Map position: 20p11.2-20p11.2

Query Match
Best Local Similarity 100.0%; Score 83; DB 2; Length 206;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKML 17
187 SNKTRIDEANORATKML 203

RESULT 6
A33623
synaptosomal-associated 25K protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 05-Nov-1999
C:Accession: A33623
R:Oyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billingsley, M.; Bloom, F.E.
J. Cell Biol. 109, 3039-3052, 1989
A:Title: The identification of a novel synaptosomal-associated protein, SNAP-25, diff
A:Reference number: A33623; MUID:90078337; PMID:2592413
A:Accession: A33623
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-206 <OYL>
A:Cross-references: GB:M22012; GB:X51673; NID:g200997; PIDN:AAA61741.1; PID:g200998

Query Match
Best Local Similarity 100.0%; Score 83; DB 2; Length 206;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKML 17
187 SNKTRIDEANORATKML 203

RESULT 7
I50552
synapse protein - marbled electric ray
C:Species: Torpedo marmorata (marbled electric ray)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I50552
R:Risinger, C.; Blomqvist, A.G.; Lundell, I.; Lambertson, A.; Nassel, D.; Pteribone,
J. Biol. Chem. 268, 24408-24414, 1993
A:Title: Evolutionary conservation of synaptosome-associated protein 25 kDa (SNAP-25)
A:Reference number: A49513; MUID:94043281; PMID:8226991
A:Accession: I50552
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-210 <RIS>
A:Cross-references: GB:LI22020; NID:g431296; PIDN:AAA49284.1; PID:g431297

Query Match
Best Local Similarity 81.2%; Score 65; DB 2; Length 210;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NKTRIDEANORATKML 17
195 NKTRIDEANORATKML 210

RESULT 8
JC5512
SNARE protein 23 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999
C:Accession: JC5512
R:Araki, S.; Tamori, Y.; Kawanishi, M.; Shinoda, H.; Masugi, T.; Mori, H.; Niki, T.;
Biochem. Biophys. Res. Commun. 234, 257-262, 1997
A:Title: Inhibition of the binding of SNAP-23 to syntaxin 4 by Munc18c.
A:Reference number: JC5512; MUID:97312558; PMID:9168999
A:Accession: JC5512

```

A:Molecule type: mRNA  
A:Residues: 1-210 <ARA>  
A:Cross-references: DDBJ:AB000822; NID:92189950; PIRN:BA020345.1; PID:d1021177; PID:9218  
C:Comment: This protein is involved in the insulin-induced translocation of vesicles con

Query Match 60.2%; Score 50; DB 2; Length 210;  
Best Local Similarity 58.8%; Pred. No. 0.37;  
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 SNKTRIDEANORATKML 17  
DB 192 TNKRRIIDIANARAKKLI 208

RESULT 9  
JC5297  
vesicle-membrane fusion protein SNAP-23B - human  
C:Species: Homo sapiens (man)  
C:Date: 02-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 05-Nov-1999  
C:Accession: JC5297  
R:Mollinedo, F.; Lazo, P.A.  
Biochem. Biophys. Res. Commun. 231, 808-812, 1997  
A:Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23  
A:Reference number: JC5296; MUID:97224437; PMID:9070898  
A:Accession: JC5297  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-158 <MOU>  
A:Cross-references: GB:Y09566; NID:91924943; PIDN:CAA70761.1; PID:e290774; PID:91924944  
A:Experimental source: neutrophils  
C:Comment: This protein is involved in regulating exocytosis in human neutrophils, a

Query Match 55.4%; Score 46; DB 2; Length 158;  
Best Local Similarity 52.9%; Pred. No. 1.3;  
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 SNKTRIDEANORATKML 17  
DB 140 TNKRRIIDIANARAKKLI 156

RESULT 10  
JC5296  
vesicle-membrane fusion protein SNAP-23A - human  
C:Species: Homo sapiens (man)  
C:Date: 02-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 05-Nov-1999  
C:Accession: JC5296  
R:Mollinedo, F.; Lazo, P.A.  
Biochem. Biophys. Res. Commun. 231, 808-812, 1997  
A:Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23  
A:Reference number: JC5296; MUID:97224437; PMID:9070898  
A:Accession: JC5296  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-211 <MOU>  
A:Cross-references: GB:Y09567; NID:91924941; PIDN:CAA70760.1; PID:e290695; PID:91924942  
C:Comment: This protein is involved in regulating exocytosis in human neutrophils, a

Query Match 55.4%; Score 46; DB 2; Length 211;  
Best Local Similarity 52.9%; Pred. No. 1.8;  
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 SNKTRIDEANORATKML 17  
DB 193 TNKRRIIDIANARAKKLI 209

RESULT 11  
T29999  
hypothetical protein ZC8.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T29999

R:Latrelle, P.; Bradshaw, H.  
submitted to the EMBL Data Library, July 1996  
A:Description: The sequence of C. elegans cosmid ZC8.  
A:Reference number: Z20719  
A:Accession: T29999  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-2288 <LATV>  
A:Cross-references: EMBL:U64862; PIDN:AAB52624.1; GSPDB:GN00028; CESP:ZC8.4  
C:Genetics:  
A:Gene: CESP:ZC8.4  
A:Map position: X  
A:introns: 43/2; 80/3; 110/3; 153/2; 274/3; 738/2; 1249/1; 1392/3; 1454/1; 1602/1; 16

Query Match 55.4%; Score 46; DB 2; Length 2288;  
Best Local Similarity 60.0%; Pred. No. 25;  
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 3 KTRIDEANORATKML 17  
DB 626 KTRIDELNRRVENL 640

RESULT 12  
T26553  
hypothetical protein Y22F5A.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T26553  
R:Gardner, A.  
submitted to the EMBL Data Library, January 1998  
A:Reference number: Z20231  
A:Accession: T26553  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-234 <WIL>  
A:Cross-references: EMBL:AL021479; PIDN:CAA16322.1; GSPDB:GN00023; CESP:Y22F5A.3  
A:Experimental source: clone Y22F5A  
C:Genetics:  
A:Gene: CESP:Y22F5A.3  
A:Map position: 5  
A:introns: 51/3; 82/1; 165/2; 213/3

Query Match 53.0%; Score 44; DB 2; Length 234;  
Best Local Similarity 41.2%; Pred. No. 4.6;  
Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 1 SNKTRIDEANORATKML 17  
DB 216 SNEVAVESANKRRAKMLI 232

RESULT 13  
A33854  
outer membrane lipoprotein I precursor - Pseudomonas aeruginosa  
C:Species: Pseudomonas aeruginosa  
C:Date: 27-Feb-1990 #sequence\_revision 27-Feb-1990 #text\_change 31-Dec-2000  
C:Accession: A33854; S04834; A44834; A83288  
R:Duchene, M.; Barron, C.; Schweizer, A.; von Specht, B.U.; Domdey, H.  
J. Bacteriol. 171, 4130-4137, 1989  
A:Title: Pseudomonas aeruginosa outer membrane lipoprotein I gene: molecular cloning,  
A:Reference number: A33854; MUID:89327122; PMID:2502533  
A:Accession: A33854  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-83 <DUC>  
A:Cross-references: GB:M25761; NID:9151334; PIDN:AAA25880.1; PID:9151335  
R:Cornelis, P.; Boula, A.; Belarbi, A.; Guyonvarch, A.; Kammerer, B.; Hannaert, V.; H  
Mol. Microbiol. 3, 421-428, 1989  
A:Title: Cloning and analysis of the gene for the major outer membrane lipoprotein fr  
A:Reference number: S04834; MUID:89313294; PMID:2473376  
A:Accession: S04834

A:Molecule type: DNA  
A:Residues: 1-83 <COR>  
A:Cross-references: EMBL:X13748; NID:945344; PIDN:CAA32013.1; PID:945345  
A>Note: the authors translated the codon GAA for residue 78 as Gly  
R:Saint-Onge, A.; Romeyer, F.; Lebel, P.; Masson, L.; Brousseau, R.  
J. Gen. Microbiol. 138, 733-741, 1992  
A:Title: Specificity of the pseudomonas aeruginosa PAO1 lipoprotein I gene as a DNA probe  
A:Reference number: A44834; MUID:92268853; PMID:1588307  
A:Accession: A44834  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-83 <SAT>  
A:Cross-references: GB:X58714; GB:S36066; NID:9433509; PIDN:CAA41550.1; PID:9433510  
A:Experimental source: PAO1  
A>Note: sequence extracted from NCBI backbone (NCBIN:103666, NCBIPI:103667)  
R:Stover, C.K.; Pham, X.Q.; Ervin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Br  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larchig, K.; Lim,  
; Lory, S.; Olson, M.V  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: A83288  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-83 <STO>  
A:Cross-references: GB:AE004712; GB:AE004091; NID:99948940; PIDN:AAG06241.1; GSPDB:GN001  
A:Experimental source: strain PAO1  
C:Genetics:  
A:Gene: oprI; PA2853  
C:Keywords: lipid binding; lipoprotein; membrane protein  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-83/Product: lipoprotein I #status predicted <MAT>

Query Match 50.6%; Score 42; DB 2; Length 83;  
Best Local Similarity 72.7%; Pred. No. 3.3;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 DEANORATKML 17  
DB 67 DEANERATKML 77

RESULT 14  
E81436  
Transmembrane transport protein Cj0182 [Imported] - Campylobacter jejuni (strain NCTC 11  
C:Species: Campylobacter jejuni  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 03-Jun-2002  
C:Accession: E81436  
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Basham, D.; Chillit  
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; Vanyilec, A.; Whitehead, S.; Barrell  
Nature 403, 665-668, 2000  
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyf  
A:Reference number: A81250; MUID:20150912; PMID:10688204  
A:Accession: E81436  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-401 <PAR>  
A:Cross-references: GB:AL139074; GB:AL111168; NID:96967505; PIDN:CAB72665.1; PID:9696767  
A:Experimental source: serotype O2, strain NCTC 11168  
C:Genetics:  
A:Gene: Cj0182  
C:Superfamily: probable inner membrane transport protein bcca

Query Match 50.6%; Score 42; DB 2; Length 401;  
Best Local Similarity 69.2%; Pred. No. 18;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 SNKTRIDEANORA 13  
DB 71 NNATLIOEANORA 83

RESULT 15

S50562  
hypothetical protein YER059w - yeast (Saccharomyces cerevisiae)  
C:Species: Saccharomyces cerevisiae  
C:Date: 28-May-1993 #sequence\_revision 24-Feb-1995 #text\_change 10-May-2001  
C:Accession: S50562  
R:Dietrich, F.S.  
Submitted to the EMBL Data Library, December 1994  
A:Description: The sequence of S. cerevisiae lambda clones 6592, 4678, 4742, and 3612  
A:Reference number: S50427  
A:Accession: S50562  
A:Molecule type: DNA  
A:Residues: 1-420 <DLE>  
A:Cross-references: EMBL:U18813; NID:91381127; PIDN:AAB64595.1; PID:9603295; MIPS:YER  
C:Genetics:  
A:Gene: SGD:PC16  
A:Cross-references: SGD:S0000861; MIPS:YER059w  
A:Map position: 5R

Query Match 50.6%; Score 42; DB 2; Length 420;  
Best Local Similarity 50.0%; Pred. No. 19;  
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 1 SNKTRIDEANORATKM 16  
DB 283 SNESLIDKANRGADKM 298

Search completed: September 16, 2003, 19:30:48  
Job time : 5.41556 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 16, 2003, 19:21:26 ; Search time 131.091 Seconds  
(without alignments)  
405.511 Million cell updates/sec

Title: US-09-942-098-2  
Perfect score: 1048  
Sequence: 1 MAEDADMRLNLEEMQRADQ.....SNKTRIDEANQRATKMLGSG 206

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1004	95.8	206	4	Q96FM2
2	1004	95.8	206	13	Q8AXM1
3	952	90.8	206	13	Q8AXM2
4	925.5	88.3	203	13	Q93579
5	906.5	86.5	181	11	P70558
6	869.5	83.0	181	11	P70557
7	703	67.1	143	6	Q9GM34
8	646	61.6	210	11	O70377
9	646	61.6	210	11	O09044
10	641	60.2	210	11	O35620
11	638.5	60.3	212	5	Q9D3L3
12	635	60.3	212	5	O76338
13	632	59.8	207	5	Q8IAE0
14	627	59.8	212	5	O44419
15	625.5	59.7	212	5	O9VH76
16	622.5	59.4	204	13	Q8JIS7

17	621	59.3	207	5	Q8IAE1	Q8IAE1 procambarius
18	607	57.9	212	5	O8T3S4	O8T3S4 loligo peal
19	601	57.3	124	13	O93578	O93578 brachydanio
20	579.5	55.3	195	5	O96574	O96574 leucophaea
21	569.5	54.3	212	5	O01389	O01389 hlrudo medi
22	540	51.5	207	5	O62414	O62414 caenorrhabi
23	476	45.4	93	4	O8IKX3	O8IKX3 homo sapien
24	405.5	38.7	132	6	O8HXZ6	O8HXZ6 oryctolagus
25	402	38.4	80	4	O9BR45	O9BR45 homo sapien
26	376.5	35.9	158	5	O96575	O96575 leucophaea
27	343.5	32.8	125	5	O96576	O96576 leucophaea
28	276.5	26.4	96	5	O96577	O96577 leucophaea
29	271	25.9	90	5	O96578	O96578 leucophaea
30	233	22.2	55	13	O93580	O93580 brachydanio
31	181	17.3	257	13	O8AVY3	O8AVY3 xenopus lae
32	172.5	16.5	260	5	O22507	O22507 caenorrhabi
33	167	15.9	419	3	O74786	O74786 schizosacch
34	164.5	15.7	284	5	O9W1I8	O9W1I8 drosophila
35	155.5	14.8	260	11	O9DBC5	O9DBC5 mus musculu
36	155.5	14.8	260	11	O9ERB0	O9ERB0 mus musculu
37	155	14.8	257	11	O9JH56	O9JH56 rattus norv
38	143	13.6	523	11	O9JHR4	O9JHR4 mus musculu
39	143	13.6	764	13	O9J4I1	O9J4I1 gallus gall
40	143	13.6	1937	6	O9TW62	O9TW62 sus scrofa
41	142.5	13.6	1931	13	O91973	O91973 coturnix co
42	140.5	13.4	891	13	O90WH5	O90WH5 gallus gall
43	140.5	13.4	1931	13	O910C5	O910C5 gallus gall
44	139.5	13.3	611	4	O14905	O14905 homo sapien
45	138	13.2	198	5	O8IEA8	O8IEA8 plasmodium

## ALIGNMENTS

### RESULT 1

Q96FM2 ID Q96FM2 PRELIMINARY; PRT; 206 AA.  
AC Q96FM2;  
DT 01-DEC-2001 (TREMREL. 19, Created)  
DT 01-DEC-2001 (TREMREL. 19, Last sequence update)  
DT 01-MAR-2003 (TREMREL. 23, Last annotation update)  
DE Similar to synaptosomal-associated protein, 25kd.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=EYE;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC010647; AHI10647.1;  
DR InterPro: IPR000928; SNAP-25.  
DR InterPro: IPR000727; T-SNARE.  
DR Pfam: PF00835; SNAP-25; 1.  
DR SMART: SM00397; T-SNARE; 2.  
DR PROSITE: P550192; T-SNARE; 2.  
SQ SEQUENCE 206 AA; 23336 MW; E272652C701EA984 CRC64;

Query Match 95.8%; Score 1004; DB 4; Length 206;  
Best local similarity 95.6%; Pred. No. 1.6e-61;  
Matches 197; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAEDADMRLNLEEMQRADQADLADSELESTRMLQLVEESKDAIRLVMDEGEQDLDRV 60  
DB 1 MAEDADMRLNLEEMQRADQADLADSELESTRMLQLVEESKDAIRLVMDEGEQDLDRV 60  
QY 61 EEGMDQINKDKAEKNTDLGKFCGICVPCNKLTSSDPYKKRANGNDDGVASQPARV 120  
DB 61 EEGMNIHNDKRAEKNTDLGKFCGICGICPCNKLTSSDPYKKRANGNDDGVASQPARV 120  
QY 121 VDREQMAISGFIIRVYNDARENMDENIEQVSGITIGRLHMLDGNEDITQNRQIDR 180  
DB 121 VDREQMAISGFIIRVYNDARENMDENIEQVSGITIGRLHMLDGNEDITQNRQIDR 180

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Db 121 VDERQMAISGGFIRRVNTDARENMEDNLEQVSGIIGNLRHMLDMGNEIDTONRQIDR 180
QY 181 IMEKADSNKTRIDEANORATKMLGSG 206
Db 181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 2
Q8AXM1 PRELIMINARY; PRT; 206 AA.
AC 08AXM1;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE SNAP25D.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kolk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF335587; AAO13789.1; -; 703B20717E577F02 CRC64;
SQ SEQUENCE 206 AA; 23187 MW; 703B20717E577F02 CRC64;

Query Match
Best Local Similarity 95.8%; Score 1004; DB 13; Length 206;
Matches 196; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 MAEDADMNLEEMQRRADQLADESLSTRMLQVESKDAGIRTLVLMDEQGEQLERI 60
Db 1 MADDADMNLEEMQRRADQLADESLSTRMLQVESKDAGIRTLVLMDEQGEQLERI 60
QY 61 EEGMDQINKDKAEKKNLTDLGKFCGLCVCPCKNLKSSDAYKKANNQDGVVASQPARV 120
Db 61 EEGMDQINKDKAEKKNLTDLGKFCGLCVCPCKNLKSSDAYKKANNQDGVVASQPARV 120
QY 121 VDERQMAISGGFIRRVNTDARENMEDNLEQVSGIIGNLRHMLDMGNEIDTONRQIDR 180
Db 121 VDERQMAISGGFIRRVNTDARENMEDNLEQVSGIIGNLRHMLDMGNEIDTONRQIDR 180
QY 181 IMEKADSNKTRIDEANORATKMLGSG 206
Db 181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 3
Q8AXM2 PRELIMINARY; PRT; 206 AA.
AC 08AXM2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE SNAP25a.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kolk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF335586; AAO13788.1; -; 2D1D0FD35E0C1DDF CRC64;
SQ SEQUENCE 206 AA; 23122 MW; 2D1D0FD35E0C1DDF CRC64;

Query Match
Best Local Similarity 90.8%; Score 952; DB 13; Length 206;
Matches 186; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MAEDADMNLEEMQRRADQLADESLSTRMLQVESKDAGIRTLVLMDEQGEQLERI 60
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Db 1 MAEDADMNLEEMQRRADQLADESLSTRMLQVESKDAGIRTLVLMDEQGEQLERI 60
QY 61 EEGMDQINKDKAEKKNLTDLGKFCGLCVCPCKNLKSSDAYKKANNQDGVVASQPARV 120
Db 61 EEGMDQINKDKAEKKNLTDLGKFCGLCVCPCKNLKSSDAYKKANNQDGVVASQPARV 120
QY 121 VDERQMAISGGFIRRVNTDARENMEDNLEQVSGIIGNLRHMLDMGNEIDTONRQIDR 180
Db 121 VDERQMAISGGFIRRVNTDARENMEDNLEQVSGIIGNLRHMLDMGNEIDTONRQIDR 180
QY 181 IMEKADSNKTRIDEANORATKMLGSG 206
Db 181 IMEKADSNKTRIDEANORATKMLGSG 206

RESULT 4
Q93579 PRELIMINARY; PRT; 203 AA.
AC 093579;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE SYNAPTOSOME-associated protein 25.2 (SYNAPTOSOME associated protein 25.2).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Ristinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
RA Larrhamar D.;
RT *Cloning of two loci for synapse protein snap25 in zebrafish:
RT comparison of paralogous linkage groups suggests loss of one locus in
RT the mammalian lineage.;
RT J. Neurosci. Res. 0:0-0(1998).
DR EMBL: AF091594; AAC64290.1; -.
DR EMBL: AF091596; AAC73007.1; -.
DR ZFIN: ZDB-GENE-980526-392; snap25b.
DR InterPro: IPR000928; SNAP-25.
DR InterPro: IPR000727; T_SNARE.
DR Pfam: PF00835; SNAP-25; 1.
DR SMART: SM00397; T_SNARE; 2.
DR PROSITE: PS0192; T_SNARE; 2.
SQ SEQUENCE 203 AA; 22647 MW; 93B7590DD0C93F38 CRC64;

Query Match
Best Local Similarity 88.3%; Score 925.5; DB 13; Length 203;
Matches 182; Conservative 8; Mismatches 13; Indels 3; Gaps 1;

QY 1 MAEDADMNLEEMQRRADQLADESLSTRMLQVESKDAGIRTLVLMDEQGEQLERI 60
Db 1 MAEDADMNLEEMQRRADQLADESLSTRMLQVESKDAGIRTLVLMDEQGEQLERI 60
QY 61 EEGMDQINKDKAEKKNLTDLGKFCGLCVCPCKNLKSSDAYKKANNQDGVVASQPARV 120
Db 61 EEGMDQINKDKAEKKNLTDLGKFCGLCVCPCKNLKSSDAYKKANNQDGVVASQPARV 117
QY 121 VDERQMAISGGFIRRVNTDARENMEDNLEQVSGIIGNLRHMLDMGNEIDTONRQIDR 180
Db 121 VDERQMAISGGFIRRVNTDARENMEDNLEQVSGIIGNLRHMLDMGNEIDTONRQIDR 177
QY 181 IMEKADSNKTRIDEANORATKMLGSG 206
Db 181 IMEKADSNKTRIDEANORATKMLGSG 203

RESULT 5
P70558 PRELIMINARY; PRT; 181 AA.
ID P70558
```



AC P70558;  
 DT 01-FEB-1997 (TReMBLrel. 02, Created)  
 DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)  
 DE 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
 DE SNAP-25b (Fragment).  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Medison D.L., Pfeiffer S.E.;  
 RT "SNARE proteins may be utilized by oligodendrocytes to assemble myelin membrane."  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, U56262; AAA9826.1; -;  
 DR InterPro: IPR000928; SNAP-25.  
 DR Pfam: PF00835; SNAP-25; 1.  
 DR SMART: SM00397; t\_SNARE; 2.  
 DR PROSITE: PS50192; t\_SNARE; 2.  
 FT NON\_TER 1  
 FT SEQUENCE 181 AA; 20585 MW; EB744A8A9A6854F8 CRC64;

Query Match 86.5%; Score 906.5; DB 11; Length 181;  
 Best Local Similarity 98.4%; Pred. No. 6.6e-55;  
 Matches 179; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 9 NEEEMORRADQDLADESLESTRRLQLVESKDGIRTLVWLDQEGQLERIEEGMQIN 68  
 || |||||  
 DB 1 NEF-EMGRADQDLADESLESTRRLQLVESKDGIRTLVWLDQEGQLERIEEGMQIN 59  
 QY 69 KDKMEAKNLTDLGKFCGLVCPCNKLSSDAYKKANGNODGVVASOPARVDERBOMA 128  
 |||||  
 DB 60 KDKMEAKNLTDLGKFCGLVCPCNKLSSDAYKKANGNODGVVASOPARVDERBOMA 119  
 QY 129 ISGFIIRVTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTONROIDRIMEKADSN 188  
 |||||  
 DB 120 ISGFIIRVTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTONROIDRIMEKADSN 179  
 QY 189 KT 190  
 ||  
 DB 180 KT 181

## RESULT 6

ID P70557 PRELIMINARY; PRT; 181 AA.  
 AC P70557;  
 DT 01-FEB-1997 (TReMBLrel. 02, Created)  
 DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)  
 DE 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
 DE SNAP-25a (Fragment).  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Medison D.L., Pfeiffer S.E.;  
 RT "SNARE proteins may be utilized by oligodendrocytes for assembling myelin membrane."  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, U56261; AAA9825.1; -;  
 DR InterPro: IPR000928; SNAP-25.  
 DR Pfam: PF00835; SNAP-25; 1.  
 DR SMART: SM00397; t\_SNARE; 2.  
 DR PROSITE: PS50192; t\_SNARE; 2.  
 FT NON\_TER 1

FT NON\_TER 181  
 SO SEQUENCE 181 AA; 20558 MW; D59CCA4BAEAD8C18 CRC64;

Query Match 83.0%; Score 869.5; DB 11; Length 181;  
 Best Local Similarity 94.5%; Pred. No. 2.3e-52;  
 Matches 172; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 9 NEEEMORRADQDLADESLESTRRLQLVESKDGIRTLVWLDQEGQLERIEEGMQIN 68  
 |||||  
 DB 1 NEF-EMGRADQDLADESLESTRRLQLVESKDGIRTLVWLDQEGQLERIEEGMQIN 59  
 QY 69 KDKMEAKNLTDLGKFCGLVCPCNKLSSDAYKKANGNODGVVASOPARVDERBOMA 128  
 :|||  
 DB 60 KDKMEAKNLTDLGKFCGLVCPCNKLSSDAYKKANGNODGVVASOPARVDERBOMA 119  
 QY 129 ISGFIIRVTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTONROIDRIMEKADSN 188  
 |||||  
 DB 120 ISGFIIRVTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTONROIDRIMEKADSN 179  
 QY 189 KT 190  
 ||  
 DB 180 KT 181

## RESULT 7

ID O9GM34 PRELIMINARY; PRT; 143 AA.  
 AC O9GM34;  
 DT 01-MAR-2001 (TReMBLrel. 16, Created)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
 DE 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
 DE Hypothetical 16.0 kDa protein.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 CC Cercopithecinae; Macaca.  
 NX NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,  
 RA Suzuki Y., Sugano S., Hashimoto K.;  
 RT "Isolation of full-length cDNA clones from macaque brain cDNA libraries."  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, AB049852; BAB16738.1; -;  
 DR InterPro: IPR000928; SNAP-25.  
 DR InterPro: IPR000727; t\_SNARE.  
 DR Pfam: PF00835; SNAP-25; 1.  
 DR SMART: SM00397; t\_SNARE; 1.  
 DR PROSITE: PS50192; t\_SNARE; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 143 AA; 16043 MW; D625DBA0A0933FB0 CRC64;

Query Match 67.1%; Score 703; DB 6; Length 143;  
 Best Local Similarity 95.1%; Pred. No. 4.6e-41;  
 Matches 136; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 64 MDQINKMEKAEKNLTDLGKFCGLVCPCNKLSSDAYKKANGNODGVVASOPARVDE 123  
 |||||  
 DB 1 MNHINQDKMEKAEKNLTDLGKFCGLVCPCNKLSSDAYKKANGNODGVVASOPARVDE 60  
 QY 124 REQMAISGFIIRVTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTONROIDRIME 183  
 |||||  
 DB 61 REQMAISGFIIRVTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTONROIDRIME 120  
 QY 184 KADSNKTRIDEANQRAATKMLGSG 206  
 |||||  
 DB 121 KADSNKTRIDEANQRAATKMLGSG 143

## RESULT 8

070377

ID 070377 PRELIMINARY; PRT; 210 AA.  
 AC 070377;  
 DT 01-AUG-1998 (TREMBlrel. 07, Created)  
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE SNAP-23.  
 GN SNAP-23.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99162237; PubMed=10051443;  
 RA St-Denis J.F., Cabaniols J.P., Cushman S.W., Roche P.A.;  
 RT "SNAP-23 participates in SNARE complex assembly in rat adipose  
 cells.";  
 RL Biochem. J. 338:709-715(1999).  
 DR EMBL: AF052596; AAC06031.1; -;  
 DR InterPro: IPR000928; SNAP-25.  
 DR Pfam: PF00835; SNAP-25; 1.  
 DR SMART: SM00397; t-SNARE; 2.  
 DR PROSITE: PS50192; t-SNARE; 2.  
 SQ SEQUENCE 210 AA; 23235 MW; 0D63E3A6F9FE3BA2 CRC64;

Query Match 61.6%; Score 646; DB 11; Length 210;  
 Best Local Similarity 62.7%; Pred. No. 5.7e-37;  
 Matches 128; Conservative 31; Mismatches 35; Indels 10; Gaps 3;

QY 12 EEMORRADOADESLESTRRLQVLEESKDACIRFLVLMDEGEOLEIEEGMDQINKDM 71  
 DB 7 EEOICRAHQVYDESLESTRRIIGLAEISQDAGIKRTITMDEGEOLEIEEGMDQINKDM 66  
 QY 72 KAEKNTLDLGFECGICVCPCKIKSSDA---YKRWGNOD---GYVASQPARVYDER 124  
 DB 67 REAEKTLTELNKCGLICPCNRTKNFEESGKNKATWGGGSDSPSNVSKOPSRITNGQ 126  
 QY 125 EOM---AISGFIIRYTDNARENEMDENLEQVSGIIGNLRHMLDGNEDIDTQNRQIDRI 181  
 DB 127 PQOTGAASGGYIKRTITNAREDEMEENTQVSGISLGNLKNMALDGNEDIDQNOQIQIKI 186  
 QY 182 MEKADSNKTRIDEANORATKMLGS 205  
 DB 187 TEKADTNKNRIDIANTRAKKLIDS 210  
 RESULT 9  
 ID 009044 PRELIMINARY; PRT; 210 AA.  
 AC 009044;  
 DT 01-JUL-1997 (TREMBlrel. 04, Created)  
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE SYNDET (SNAP-23) (Synapcosomal-associated protein, 23KD).  
 GN SNAP23 OR SNT.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Fat;  
 RX MEDLINE=97312558; PubMed=9168999;  
 RA Araki S., Tamori Y., Kawanishi M., Shioda H., Masugi J., Mori H.,  
 RA Niki T., Okazawa H., Kubota T., Kasuga M.;  
 RT "Inhibition of the binding of SNAP-23 to syntaxin 4 by Munc18c.";  
 RL Biochem. Biophys. Res. Commun. 234:257-262(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97220227; PubMed=9067602;  
 RA Wang G., Wilkin J.W., Hao G., Bankaitis V.A., Scherer P.E.,  
 RA Baldini G.;

RT "SynDET is a novel SNAP-25 related protein expressed in many  
 tissues.";  
 RT J. Cell Sci. 110:505-513(1997).  
 RL [3]  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SVJ;  
 RA Vaidyanathan V.V., Roche P.A.;  
 RT "Structure and chromosomal localization of the mouse SNAP-23 gene.";  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Embryo;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Glass C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsch G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita K., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata J., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 DR EMBL: AB000822; BAA20345.1; -;  
 DR EMBL: U73143; AAB53597.1; -;  
 DR EMBL: AF213237; AAF23503.1; -;  
 DR EMBL: AF213251; AAF23503.1; JOINED.  
 DR EMBL: AF213252; AAF23503.1; JOINED.  
 DR EMBL: AF213253; AAF23503.1; JOINED.  
 DR EMBL: AF213254; AAF23503.1; JOINED.  
 DR EMBL: AF213255; AAF23503.1; JOINED.  
 DR EMBL: AF213256; AAF23503.1; JOINED.  
 DR EMBL: AK018162; BAB31577.1; -;  
 DR MGD; MGI:109356; Snap23.  
 DR InterPro: IPR000928; SNAP-25.  
 DR InterPro: IPR000727; t-SNARE.  
 DR Pfam: PF00835; SNAP-25; 1.  
 DR SMART: SM00397; t-SNARE; 2.  
 DR PROSITE: PS50192; t-SNARE; 2.  
 SQ SEQUENCE 210 AA; 23261 MW; 6919E127E16BA2C9 CRC64;

Query Match 61.6%; Score 646; DB 11; Length 210;  
 Best Local Similarity 62.3%; Pred. No. 5.7e-37;  
 Matches 127; Conservative 32; Mismatches 35; Indels 10; Gaps 3;

QY 12 EEMORRADOADESLESTRRLQVLEESKDACIRFLVLMDEGEOLEIEEGMDQINKDM 71  
 DB 7 EEOVLAHQVYDESLESTRRIIGLAEISQDAGIKRTITMDEGEOLEIEEGMDQINKDM 66  
 QY 72 KAEKNTLDLGFECGICVCPCKIKSSDA---YKRWGNOD---NNQDGYVASQPARVYDER 124  
 DB 67 REAEKTLTELNKCGLICPCNRTKNFEESGKNKATWGGGSDSPSNVSKOPSRITNGQ 126  
 QY 125 EOM---AISGFIIRYTDNARENEMDENLEQVSGIIGNLRHMLDGNEDIDTQNRQIDRI 181  
 DB 127 PQOTGAASGGYIKRTITNAREDEMEENTQVSGISLGNLKNMALDGNEDIDQNOQIQIKI 186  
 QY 182 MEKADSNKTRIDEANORATKMLGS 205  
 DB 187 TEKADTNKNRIDIANTRAKKLIDS 210

RESULT 10







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OM protein - protein search, using sw model

Run on: September 16, 2003, 19:23:56 : Search time 4.41558 seconds  
(without alignments)  
573.239 Million cell updates/sec

Title: US-09-942-098-2\_COPY\_187\_203

Perfect score: 83  
Sequence: 1 SNKTRIDEANORATKML 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 556269 seqs, 148893369 residues

Total number of hits satisfying chosen parameters: 556269

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Published\_Applications\_AA.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	83	100.0	17	US-09-942-098-30	Sequence 30, Appl
3	83	100.0	17	US-10-011-568-2	Sequence 2, Appl
4	83	100.0	18	US-09-942-024-32	Sequence 32, Appl
5	83	100.0	18	US-09-942-098-32	Sequence 32, Appl
6	83	100.0	21	US-09-942-024-85	Sequence 89, Appl
7	83	100.0	21	US-09-942-098-89	Sequence 89, Appl
8	83	100.0	23	US-09-942-024-88	Sequence 88, Appl
9	83	100.0	23	US-09-942-098-88	Sequence 88, Appl
10	83	100.0	24	US-09-942-024-90	Sequence 90, Appl
11	83	100.0	24	US-09-942-098-90	Sequence 90, Appl
12	83	100.0	33	US-09-942-024-33	Sequence 33, Appl
13	83	100.0	33	US-09-942-024-37	Sequence 37, Appl
14	83	100.0	33	US-09-942-024-38	Sequence 38, Appl
15	83	100.0	33	US-09-942-098-33	Sequence 33, Appl

16	83	100.0	33	US-09-942-098-37	Sequence 37, Appl
17	83	100.0	33	US-09-942-098-38	Sequence 38, Appl
18	83	100.0	116	US-09-962-360B-11	Sequence 11, Appl
19	83	100.0	203	US-09-942-024-14	Sequence 14, Appl
20	83	100.0	203	US-09-942-098-14	Sequence 14, Appl
21	83	100.0	206	US-09-942-024-2	Sequence 2, Appl
22	83	100.0	206	US-09-942-024-7	Sequence 7, Appl
23	83	100.0	206	US-09-942-024-12	Sequence 12, Appl
24	83	100.0	206	US-09-942-098-2	Sequence 2, Appl
25	83	100.0	206	US-09-942-098-12	Sequence 12, Appl
26	83	100.0	206	US-09-942-098-12	Sequence 12, Appl
27	80	96.4	17	US-09-942-024-55	Sequence 55, Appl
28	80	96.4	17	US-09-942-098-55	Sequence 55, Appl
29	79	95.2	16	US-09-942-024-29	Sequence 29, Appl
30	79	95.2	16	US-09-942-098-29	Sequence 29, Appl
31	79	95.2	17	US-09-942-024-31	Sequence 31, Appl
32	79	95.2	17	US-09-942-024-47	Sequence 47, Appl
33	79	95.2	17	US-09-942-024-49	Sequence 49, Appl
34	79	95.2	17	US-09-942-024-54	Sequence 54, Appl
35	79	95.2	17	US-09-942-098-31	Sequence 31, Appl
36	79	95.2	17	US-09-942-098-47	Sequence 47, Appl
37	79	95.2	17	US-09-942-098-49	Sequence 49, Appl
38	79	95.2	17	US-09-942-098-54	Sequence 54, Appl
39	79	95.2	19	US-09-942-024-85	Sequence 85, Appl
40	79	95.2	19	US-09-942-098-85	Sequence 85, Appl
41	78	94.0	17	US-09-942-024-48	Sequence 48, Appl
42	78	94.0	17	US-09-942-024-52	Sequence 52, Appl
43	78	94.0	17	US-09-942-024-56	Sequence 56, Appl
44	78	94.0	17	US-09-942-098-48	Sequence 48, Appl
45	78	94.0	17	US-09-942-098-52	Sequence 52, Appl

#### ALIGNMENTS

RESULT 1  
US-09-942-024-30  
; Sequence 30, Application US/09942024  
; Publication No. US20030143650A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
; FILE REFERENCE: P-AR 4803  
; CURRENT APPLICATION NUMBER: US/09/942,024  
; CURRENT FILING DATE: 2001-08-28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-942-024-30

Query Match 100.0% Score 83; DB 12; Length 17;  
Best Local Similarity 100.0%; Pred. No. 7e-08; 0; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 0;

QY 1 SNKTRIDEANORATKML 17  
|||||  
Db 1 SNKTRIDEANORATKML 17

RESULT 2  
US-09-942-098-30  
; Sequence 30, Application US/09942098  
; Publication No. US20030143651A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger

;; TITLE OF INVENTION: Fret Protease Assays For Clostridial  
;; FILE REFERENCE: Toxins  
;; CURRENT APPLICATION NUMBER: US/09/942,098  
;; CURRENT FILING DATE: 2001-08-28  
;; NUMBER OF SEQ ID NOS: 96  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 30  
;; LENGTH: 17  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-942-098-30

Query Match 100.0%; Score 83; DB 12; Length 17;  
Best Local Similarity 100.0%; Pred. No. 7e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKML 17  
Db 1 SNKTRIDEANORATKML 17

## RESULT 3

US-10-011-588-2  
;; Sequence 2, Application US/10011588  
;; Publication No. US2002016872A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Jensen, Melody  
;; APPLICANT: Jensen, Leonard  
;; TITLE OF INVENTION: RECOMBINANT LIGHT CHAINS OF BOTULINUM  
;; TITLE OF INVENTION: NEUROTOXINS AND LIGHT CHAIN FUSION PROTEINS FOR USE IN  
;; FILE REFERENCE: A34796 067252.0113  
;; CURRENT APPLICATION NUMBER: US/10/011,588  
;; CURRENT FILING DATE: 2002-03-29  
;; PRIOR APPLICATION NUMBER: 09/910,186  
;; PRIOR FILING DATE: 2001-07-20  
;; PRIOR APPLICATION NUMBER: 09/611,419  
;; PRIOR FILING DATE: 2000-07-06  
;; PRIOR APPLICATION NUMBER: 60/246,744  
;; PRIOR FILING DATE: 2000-11-06  
;; PRIOR APPLICATION NUMBER: 60/311,966  
;; PRIOR FILING DATE: 2001-08-09  
;; NUMBER OF SEQ ID NOS: 47  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 2  
;; LENGTH: 17  
;; TYPE: PRT  
;; ORGANISM: Human  
;; FEATURE:  
;; NAME/KEY: PEPTIDE  
;; LOCATION: (0)...(0)  
;; OTHER INFORMATION: Residues 187-203 of SNAP-25  
US-10-011-588-2

Query Match 100.0%; Score 83; DB 14; Length 17;  
Best Local Similarity 100.0%; Pred. No. 7e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKML 17  
Db 1 SNKTRIDEANORATKML 17

## RESULT 4

US-09-942-024-32  
;; Sequence 32, Application US/09942024  
;; Publication No. US20030143650A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Steward, Lance E.  
;; APPLICANT: Fernandez-Salas, Ester  
;; APPLICANT: Aoki, Kei Roger  
;; TITLE OF INVENTION: Fret Protease Assays For Botulinum

;; TITLE OF INVENTION: Serotype A/E Toxins  
;; FILE REFERENCE: P-AR 4803  
;; CURRENT APPLICATION NUMBER: US/09/942,024  
;; CURRENT FILING DATE: 2001-08-28  
;; NUMBER OF SEQ ID NOS: 96  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 32  
;; LENGTH: 18  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-942-024-32

Query Match 100.0%; Score 83; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.5e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKML 17  
Db 2 SNKTRIDEANORATKML 18

## RESULT 5

US-09-942-098-32  
;; Sequence 32, Application US/09942098  
;; Publication No. US20030143651A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Steward, Lance E.  
;; APPLICANT: Fernandez-Salas, Ester  
;; APPLICANT: Aoki, Kei Roger  
;; TITLE OF INVENTION: Fret Protease Assays For Clostridial  
;; TITLE OF INVENTION: Toxins  
;; FILE REFERENCE: P-AR 4802  
;; CURRENT APPLICATION NUMBER: US/09/942,098  
;; CURRENT FILING DATE: 2001-08-28  
;; NUMBER OF SEQ ID NOS: 96  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 32  
;; LENGTH: 18  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-942-098-32

Query Match 100.0%; Score 83; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.5e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKML 17  
Db 2 SNKTRIDEANORATKML 18

## RESULT 6

US-09-942-024-89  
;; Sequence 89, Application US/09942024  
;; Publication No. US20030143650A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Steward, Lance E.  
;; APPLICANT: Fernandez-Salas, Ester  
;; APPLICANT: Aoki, Kei Roger  
;; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
;; TITLE OF INVENTION: Serotype A/E Toxins  
;; FILE REFERENCE: P-AR 4803  
;; CURRENT APPLICATION NUMBER: US/09/942,024  
;; CURRENT FILING DATE: 2001-08-28  
;; NUMBER OF SEQ ID NOS: 96  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 89  
;; LENGTH: 21  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: synthetic peptide  
;; NAME/KEY: MOD\_RES



```
/ LOCATION: 1
/ OTHER INFORMATION: Xaa=fluorescein-modified lysine
/ NAME/KEY: MOD_RES
/ LOCATION: 21
/ OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
/ NAME/KEY: AMIDATION
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: at the C-terminal
US-09-942-024-89
```

```
Query Match          100.0%; Score 83; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SNKTRIDEANORATKML 17
         |||
Db      4 SNKTRIDEANORATKML 20
```

## RESULT 7

```
US-09-942-098-89
; Sequence 89, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 21
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-89
```

```
Query Match          100.0%; Score 83; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SNKTRIDEANORATKML 17
         |||
Db      4 SNKTRIDEANORATKML 20
```

## RESULT 8

```
US-09-942-024-88
; Sequence 88, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
```

```
/ NUMBER OF SEQ ID NOS: 96
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 88
/ LENGTH: 23
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
/ NAME/KEY: MOD_RES
/ LOCATION: 1
/ OTHER INFORMATION: Xaa=fluorescein-modified lysine
/ NAME/KEY: MOD_RES
/ LOCATION: 23
/ OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
/ NAME/KEY: AMIDATION
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: at the C-terminal
US-09-942-024-88
```

```
Query Match          100.0%; Score 83; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SNKTRIDEANORATKML 17
         |||
Db      3 SNKTRIDEANORATKML 19
```

## RESULT 9

```
US-09-942-098-88
; Sequence 88, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 23
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-88
```

```
Query Match          100.0%; Score 83; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.9e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 SNKTRIDEANORATKML 17
         |||
Db      3 SNKTRIDEANORATKML 19
```

## RESULT 10

```
US-09-942-024-90
; Sequence 90, Application US/09942024
; Publication No. US20030143650A1
```

```

: GENERAL INFORMATION:
: APPLICANT: Steward, Lance E.
: APPLICANT: Fernandez-Salas, Ester
: APPLICANT: Aoki, Kei Roger
: TITLE OF INVENTION: FRET Protease Assays For Botulinum
: FILE REFERENCE: P-AR 4803
: CURRENT APPLICATION NUMBER: US/09/942,024
: NUMBER OF SEQ ID NOS: 96
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 90
: LENGTH: 24
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: synthetic peptide
: NAME/KEY: MOD_RES
: LOCATION: 1
: OTHER INFORMATION: Xaa-fluorescein-modified lysine
: NAME/KEY: MOD_RES
: LOCATION: 24
: OTHER INFORMATION: Xaa-tetramethylrhodamine-modified lysine
: NAME/KEY: AMIDATION
: LOCATION: (0)...(0)
: OTHER INFORMATION: at the C-terminal
US-09-942-024-90

```

```

Query Match          100.0%; Score 83; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  SNKTRIDEANORATKML 17
        |||
Db      4  SNKTRIDEANORATKML 20

```

```

RESULT 11
US-09-942-098-90
: Sequence 90, Application US/09942098
: Publication No. US20030143651A1
: GENERAL INFORMATION:
: APPLICANT: Steward, Lance E.
: APPLICANT: Fernandez-Salas, Ester
: APPLICANT: Aoki, Kei Roger
: TITLE OF INVENTION: FRET Protease Assays For Clostridia
: FILE REFERENCE: P-AR 4802
: CURRENT APPLICATION NUMBER: US/09/942,098
: CURRENT FILING DATE: 2001-08-28
: NUMBER OF SEQ ID NOS: 96
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 90
: LENGTH: 24
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: synthetic peptide
: NAME/KEY: MOD_RES
: LOCATION: 1
: OTHER INFORMATION: Xaa-fluorescein-modified lysine
: NAME/KEY: MOD_RES
: LOCATION: 24
: OTHER INFORMATION: Xaa-tetramethylrhodamine-modified lysine
: NAME/KEY: AMIDATION
: LOCATION: (0)...(0)
: OTHER INFORMATION: at the C-terminal
US-09-942-098-90

```

```

Query Match          100.0%; Score 83; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  SNKTRIDEANORATKML 17
        |||
Db      4  SNKTRIDEANORATKML 20

```

```

RESULT 12
US-09-942-024-33
: Sequence 33, Application US/09942024
: Publication No. US20030143650A1
: GENERAL INFORMATION:
: APPLICANT: Steward, Lance E.
: APPLICANT: Fernandez-Salas, Ester
: APPLICANT: Aoki, Kei Roger
: TITLE OF INVENTION: FRET Protease Assays For Botulinum
: FILE REFERENCE: P-AR 4803
: CURRENT APPLICATION NUMBER: US/09/942,024
: CURRENT FILING DATE: 2001-08-28
: NUMBER OF SEQ ID NOS: 96
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 33
: LENGTH: 33
: TYPE: PRT
: ORGANISM: Mus musculus
US-09-942-024-33

```

```

Query Match          100.0%; Score 83; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  SNKTRIDEANORATKML 17
        |||
Db      14 SNKTRIDEANORATKML 30

```

```

RESULT 13
US-09-942-024-37
: Sequence 37, Application US/09942024
: Publication No. US20030143650A1
: GENERAL INFORMATION:
: APPLICANT: Steward, Lance E.
: APPLICANT: Fernandez-Salas, Ester
: APPLICANT: Aoki, Kei Roger
: TITLE OF INVENTION: FRET Protease Assays For Botulinum
: FILE REFERENCE: P-AR 4803
: CURRENT APPLICATION NUMBER: US/09/942,024
: CURRENT FILING DATE: 2001-08-28
: NUMBER OF SEQ ID NOS: 96
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 37
: LENGTH: 33
: TYPE: PRT
: ORGANISM: Carassius auratus
US-09-942-024-37

```

```

Query Match          100.0%; Score 83; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  SNKTRIDEANORATKML 17
        |||
Db      14 SNKTRIDEANORATKML 30

```

```

RESULT 14
US-09-942-024-38
: Sequence 38, Application US/09942024
: Publication No. US20030143650A1
: GENERAL INFORMATION:
: APPLICANT: Steward, Lance E.
: APPLICANT: Fernandez-Salas, Ester
: APPLICANT: Aoki, Kei Roger

```

```
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-024-38
```

```
Query Match          100.0%; Score 83; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 SNKTRIDEANORATKML 17
        |||
Db      14 SNKTRIDEANORATKML 30
```

```
RESULT 15
US-09-942-098-33
; Sequence 33, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-098-33
```

```
Query Match          100.0%; Score 83; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 SNKTRIDEANORATKML 17
        |||
Db      14 SNKTRIDEANORATKML 30
```

```
Search completed: September 16, 2003, 19:31:53
Job time : 4.4158 secs
```

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OW protein - protein search, using sw model

Run on: September 16, 2003, 19:11:00 ; Search time 12.1429 Seconds  
(without alignments)  
222.217 Million cell updates/sec

Title: US-09-942-098-2\_COPY\_187\_203

Perfect score: 83

Sequence: 1 SNKTRIDEANQGRATKML 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_19Jun03: \*

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT: \*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT: \*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT: \*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT: \*
- 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT: \*
- 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT: \*
- 7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT: \*
- 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT: \*
- 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT: \*
- 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT: \*
- 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT: \*
- 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT: \*
- 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT: \*
- 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT: \*
- 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT: \*
- 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT: \*
- 17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT: \*
- 18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT: \*
- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT: \*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT: \*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT: \*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT: \*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT: \*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	17	20	AAV44021
2	83	100.0	17	20	AAV44057
3	83	100.0	17	23	ABG69065
4	83	100.0	19	22	AAAB15586
5	83	100.0	20	18	AAW30100
6	83	100.0	25	18	AAW30099
7	83	100.0	37	18	AAW30097
8	83	100.0	70	17	AAAB6823
9	83	100.0	86	22	AAAB15584

10	83	100.0	116	23	AAO15165	Clostridial neurot
11	83	100.0	206	18	AAW30103	Synaptosomal assoc
12	83	100.0	206	19	AAW79198	Mouse SNAP-25 poly
13	83	100.0	206	19	AAW43426	Mouse synaptosomal
14	83	100.0	206	22	AAU00246	Synaptosomal-assoc
15	83	100.0	206	22	AAU00252	SNARE homologue, s
16	83	100.0	206	22	AAU00253	SNARE homologue, s
17	80	96.4	17	20	AAV44038	Human SNAP25 (amin
18	80	96.4	17	20	AAV44063	Human SNAP25 (amin
19	79	95.2	16	20	AAV44069	Human SNAP25 (amin
20	79	95.2	17	20	AAV44047	Human SNAP25 (amin
21	79	95.2	17	20	AAV44050	Human SNAP25 (amin
22	79	95.2	17	20	AAV44052	Human SNAP25 (amin
23	79	95.2	17	20	AAV44059	Human SNAP25 (amin
24	78	95.2	206	22	AAU02640	Synaptosomal-assoc
25	78	94.0	17	20	AAV44039	Human SNAP25 (amin
26	78	94.0	17	20	AAV44045	Human SNAP25 (amin
27	78	94.0	17	20	AAV44049	Human SNAP25 (amin
28	78	94.0	17	20	AAV44062	Human SNAP25 (amin
29	78	94.0	17	20	AAV44070	Human SNAP25 (amin
30	77	92.8	17	20	AAV44022	Human SNAP25 (amin
31	77	92.8	17	20	AAV44040	Human SNAP25 (amin
32	77	92.8	17	20	AAV44044	Human SNAP25 (amin
33	77	92.8	17	20	AAV44046	Human SNAP25 (amin
34	77	92.8	17	20	AAV44048	Human SNAP25 (amin
35	77	92.8	17	20	AAV44051	Human SNAP25 (amin
36	77	92.8	17	20	AAV44053	Human SNAP25 (amin
37	77	92.8	17	20	AAV44054	Human SNAP25 (amin
38	77	92.8	17	20	AAV44056	Human SNAP25 (amin
39	77	92.8	17	20	AAV44064	Human SNAP25 (amin
40	77	92.8	17	20	AAV44065	Human SNAP25 (amin
41	77	92.8	17	20	AAV44066	Human SNAP25 (amin
42	77	92.8	24	23	AAO15162	Clostridial neurot
43	77	92.8	116	23	AAO15166	Clostridial neurot
44	77	92.8	203	22	AAU02636	Synaptosomal-assoc
45	77	92.8	206	22	AAU00259	Synaptosomal-assoc

#### ALIGNMENTS

RESULT 1	
AAV44021	
ID	AAV44021 standard; peptide: 17 AA.
AC	AAV44021;
XX	
DT	18-JAN-2000 (first entry)
DE	Amino acids 187-203 of human SNAP25.
XX	
KW	Enzymatic assay; quantitation: type A botulinum neurotoxin; proteolysis;
KW	fluorescamine; detection: human; synaptosomal protein; SNAP25;
KW	hydrolysis; amino group.
XX	
OS	Homo sapiens.
XX	
PN	US5965699-A.
XX	
PD	12-OCT-1999.
XX	
PF	06-NOV-1996; 96US-0743894.
XX	
PR	06-NOV-1996; 96US-0743894.
XX	
PA	(USSA ) US SEC OF ARMY.
XX	
PI	Bostian KA, Schmidt JF;
XX	
DR	WPI: 1999-579939/49.
XX	
PT	Quantitation of type A botulinum toxin -
XX	

PS Claim 1; Column 4; 28pp; English.

XX The invention relates to an enzymatic assay for the quantitation of

CC type A botulinum toxin, by determining the proteolytic activity of

CC botulinum neurotoxin type A using fluorescamine detection. The method

CC comprises adding an analogue (e.g. AAY44022-Y44076) of this peptide

CC (which represents amino acids 187-203 of the human synaptosomal protein

CC SNAP25) to a sample containing the botulinum toxin A so that hydrolysis

CC of the peptide is initiated, then stopping hydrolysis of the peptide at

CC different time points; and measuring the amount of hydrolysis at each

CC time point by combining with a label capable of detecting free amino

CC groups resulting from the hydrolysis. The amount of botulinum toxin A

CC present in the sample is determined by comparing measurements with the

CC amount of label produced from a known concentration of toxin measured

CC under similar conditions. The method is useful for the quantitation of

CC type A botulinum toxin.

XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 83; DB 20; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.1e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SNKTRIDEANORATKML 17

Db 1 SNKTRIDEANORATKML 17

RESULT 2

AAY44057

ID AAY44057 standard; peptide; 17 AA.

XX AAY44057;

XX 18-JAN-2000 (first entry)

DE Human SNAP25 (amino acids 187-203) analogue #36.

XX

KW Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis;

KW fluorescamine; detection; human; synaptosomal protein; SNAP25;

KW hydrolysis; amino group.

OS Homo sapiens.

OS Synthetic.

PN US5965699-A.

XX 12-OCT-1999.

PD

XX 06-NOV-1996; 96US-0743894.

PF

XX 06-NOV-1996; 96US-0743894.

PR

XX 06-NOV-1996; 96US-0743894.

XX

PA (USSA ) US SEC OF ARMY.

XX

PI Bostian KA, Schmidt JJ;

XX

DR WPI; 1999-579939/49.

XX

PT Quantitation of type A botulinum toxin -

PS Disclosure; Column 9; 28pp; English.

XX

CC The invention relates to an enzymatic assay for the quantitation of

CC type A botulinum toxin, by determining the proteolytic activity of

CC botulinum neurotoxin type A using fluorescamine detection. Botulinum

CC toxin A has been shown to cleave the synaptosomal neurotransmitter

CC peptide SNAP25 between residues 197-198. The method comprises adding

CC an analogue (e.g. AAY44022-Y44076) of the SNAP25 peptide (AAY44021,

CC amino acids 187-203 of human SNAP25) to a sample containing the

CC botulinum toxin A so that hydrolysis of the peptide is initiated, then

CC stopping hydrolysis of the peptide at different time points; and

CC measuring the amount of hydrolysis at each time point by combining with a

CC label capable of detecting free amino groups resulting from the

CC hydrolysis. The amount of botulinum toxin A present in the sample is

CC determined by comparing measurements with the amount of label produced

CC from a known concentration of toxin measured under similar conditions.

CC The method is useful for the quantitation of type A botulinum toxin.

XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 83; DB 20; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.1e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SNKTRIDEANORATKML 17

Db 1 SNKTRIDEANORATKML 17

RESULT 3

ABG69065

ID ABG69065 standard; peptide; 17 AA.

XX ABG69065;

XX 07-OCT-2002 (first entry)

DE Human polypeptide C-terminal fragment.

XX

KW Botulinum neurotoxin light chain; BoNT LC; botulism; dystonia; pain;

KW spasticity; ocular motility; facial dyskinesia; stiff-person syndrome;

KW bladder dysfunction; segmental myoclonus; hyperkinetic disorder; human;

KW cosmetic treatment; facial wrinkle; cerebral palsy; analgesic; relaxant;

KW lower motor neuron hyperactivity; autonomic nerve function; muscular;

XX immunostimulant; antibacterial.

XX

OS Homo sapiens.

PN WO200236758-A2.

XX 10-MAY-2002.

PD

XX 06-NOV-2001; 2001WO-US47230.

PF

XX 06-NOV-2000; 2000US-246774P.

PR 20-JUL-2001; 2001US-0910186.

PR 09-AUG-2001; 2001US-311966P.

XX

PA (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.

XX

PI Smith LA, Jensen M;

XX

DR WPI; 2002-575192/61.

XX

PT Novel nucleic acid molecule encoding botulinum neurotoxin light chain

PT serotype A, useful for producing the neurotoxin for vaccination against

PT botulism, comprises sequence expressible in host other than Clostridium

XX

XX Example 25; Page 62; 166pp; English.

XX

CC The invention relates to a nucleic acid molecule encoding a botulinum

CC neurotoxin light chain (BoNT LC) serotype A, where the DNA has a sequence

CC that is expressible in a host organism other than Clostridium, or has a

CC total A-T content that is less than about 70% The BoNT LC protein is

CC useful in vaccination against botulism, for eliciting protective immunity

CC in a mammal, for treating dystonias, spasticity, pain, ocular motility,

CC facial dyskinesias, stiff-person syndrome, bladder dysfunction, segmental

CC myoclonus, hyperkinetic disorders, cosmetic treatment of facial wrinkles,

CC conditions characterised by hyperactivity of the lower motor neuron, and

CC to control autonomic nerve function or lip toe-walking due to stiff

CC muscles common in children with cerebral palsy. The sequences are also

CC useful for screening for botulinum neurotoxin inhibitors. This sequence

CC represents a human polypeptide C-terminal fragment, used in the scope of

CC the invention.

```

XX Sequence 17 AA:
SQ
Query Match 100.0%; Score 83; DB 23; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SNKTRIDEANORATKML 17
DB 1 SNKTRIDEANORATKML 17

RESULT 4
AAB15586 standard; peptide; 19 AA.
XX
AC AAB15586;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human SNAP-25 N-terminal peptide #6.
XX
KW Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;
KW SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;
KW neurodegenerative disorder.
XX
OS Homo sapiens.
XX
PN WO200064932-A1.
XX
PD 02-NOV-2000.
XX
PE 18-FEB-2000; 2000WO-ES00058.
XX
PR 23-APR-1999; 99ES-0000844.
XX
PA (LIPO-) LIPOTEC SA.
XX
PI Blanes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;
PI Fernandez Ballesster GJ, Planell Cases RM, Ferrer Montiel AV;
PI Vinyera Boyer S, Gutierrez Perez LM, Carbonell Castell T;
PI Perez Paya E;
XX
DR WPI; 2001-007091/01.
XX
PT New peptides containing amino acid sequences from known proteins for
PT treatment of neurological disorders
XX
PS Claim 17; Page 34; 40pp; Spanish.
XX
CC The invention relates to new peptides comprising 3-30 contiguous amino
CC acids from the N-terminus of the protein SNAP-25
CC (synaptosomal-associated protein 25). The peptides AAB15581-B15586
CC represent examples of the peptides of the invention. The peptides have
CC neuronal exocytosis inhibitory activity and are used for treatment of
CC facial wrinkles and asymmetry and pathological neuronal
CC exocytosis-mediated pathological disorders and alterations manifested
CC e.g. by spasms and neurological and neurodegenerative disorders.
XX
SQ Sequence 19 AA:
Query Match 100.0%; Score 83; DB 22; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SNKTRIDEANORATKML 17
DB 3 SNKTRIDEANORATKML 19

RESULT 5
AAM30100 standard; peptide; 20 AA.
ID AAM30100

```

```

XX AAM30100;
AC
XX
DT 06-APR-1998 (first entry)
XX
DE Neurotransmitter secretion inhibitor #4.
XX
KW Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;
KW excitation-secretory uncoupling peptide; catecholamine secretion;
KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;
KW synaptosomal associated protein; SNAP-25.
XX
OS Homo sapiens.
XX
PN WO9734620-A1.
XX
PD 25-SEP-1997.
XX
PE 18-MAR-1997; 97WO-US04393.
XX
PR 18-MAR-1996; 96US-0013599.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Montal M;
XX
DR WPI; 1997-479986/44.
XX
PT Excitation-secretory uncoupling peptide(s) for inhibiting
PT neuro:transmitter release - used particularly for treating muscle
PT spasticity, and for delivering drugs specifically to neural cells
XX
PS Claim 14; Page 32; 61pp; English.
XX
CC This sequence corresponds to residues 187-206 of the human 25 kD
CC synaptosomal associated protein (SNAP-25), and is a inhibitory agent of
CC the invention. The agents of the invention inhibit secretion of
CC neurotransmitter from neuronal cells and is an excitation-secretory
CC uncoupling peptide (I) of at least 20 amino acids (aa) all of which
CC correspond substantially to any one of AAM30097-W30102, or more
CC generally any (I) that inhibits 50% of catecholamine secretion from
CC bovine chromaffin cells at a concentration of 10 microm, especially 0.25
CC microm, or less. (I) are used, as a replacement for Clostridium toxin, to
CC inhibit release of neurotransmitters from synaptic vesicles, specifically
CC for reducing muscle spasticity. Also (I) may be labelled to allow in
CC vivo imaging of intracellular distribution of (I). Compounds for
CC delivering the drug to neural cells provide targeted drug delivery, e.g.
CC of substance P to brain tumours for induction of apoptosis. Unlike the
CC neurotoxins, (I) are not toxic or immunogenic and are more readily
CC available. Their therapeutic effect lasts for several days or weeks, so
CC lower doses or less frequent treatments are required.
XX
SQ Sequence 20 AA:
Query Match 100.0%; Score 83; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SNKTRIDEANORATKML 17
DB 1 SNKTRIDEANORATKML 17

RESULT 6
AAM30099 standard; peptide; 26 AA.
ID AAM30099
XX
AC AAM30099;
XX
DT 06-APR-1998 (first entry)
XX
DE Neurotransmitter secretion inhibitor #3.
XX

```

KW	Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle; excitation-secretory uncoupling peptide; catecholamine secretion;
KW	bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;
KW	synaptosomal associated protein; SNAP-25.
XX	
OS	Homo sapiens.
XX	
PN	W09734620-A1.
XX	
PD	25-SEP-1997.
XX	
PF	18-MAR-1997; 97WO-US04393.
XX	
PR	18-MAR-1996; 96US-0013599.
XX	
PA	(REGC ) UNIV CALIFORNIA.
XX	
PI	Montal M;
XX	
DR	WPI; 1997-479986/44.
XX	
PT	Excitation-secretory uncoupling peptide(s) for inhibiting
XX	neurotransmitter release - used particularly for treating muscle
PT	spasticity, and for delivering drugs specifically to neural cells
XX	
PS	Claim 13; Page 31; 61pp; English.
XX	
CC	This sequence corresponds to residues 181-206 of the human 25 kD
XX	synaptosomal associated protein (SNAP-25), and is a inhibitory agent of
CC	the invention. The agents of the invention inhibit secretion of
XX	neurotransmitter from neuronal cells and is an excitation-secretory
CC	uncoupling peptide (1) of at least 20 amino acids (aa) all of which
XX	correspond substantially to any one of AAW30097-W30102, or more
CC	generally any (1) that inhibits 50% of catecholamine secretion from
XX	bovine chromaffin cells at a concentration of 10 microm, especially 0.25
CC	microm, or less. (1) are used, as a replacement for Clostridium toxin, to
XX	inhibit release of neurotransmitters from synaptic vesicles, specifically
CC	for reducing muscle spasticity. Also (1) may be labelled to allow in
XX	vivo imaging of intracellular distribution of (1). Compounds for
CC	delivering the drug to neural cells provide targeted drug delivery, e.g.
XX	of substance P to brain tumours for induction of apoptosis. Unlike the
CC	neurotoxins, (1) are not toxic or immunogenic and are more readily
XX	available. Their therapeutic effect lasts for several days or weeks, so
CC	lower doses or less frequent treatments are required.
XX	
SO	Sequence 26 AA:
XX	
Query Match	100.0%; Score 83; DB 18; Length 26;
Best Local Similarity	100.0%; Pred. No. 1.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 SNKTRIDEANORATKML 17
Db	7 SNKTRIDEANORATKML 23
XX	
RESULT 7	
AAW30097	
ID	AAW30097 standard; peptide: 37 AA.
XX	
AC	AAW30097:
XX	
DT	06-APR-1998 (first entry)
XX	
DE	Neurotransmitter secretion inhibitor #1.
XX	
KW	Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;
XX	excitation-secretory uncoupling peptide; catecholamine secretion;
KW	bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;
XX	synaptosomal associated protein; SNAP-25.
XX	
CS	Homo sapiens.
XX	

```

PN MO9734620-A1.
XX
XX 25-SEP-1997.
PD
XX 18-MAR-1997; 97WO-USO4393.
PF
XX 18-MAR-1996; 96US-0013599.
PR
XX (REGC ) UNIV CALIFORNIA.
PA
XX Montal M;
PI
XX WPI: 1997-479986/44.
DR
XX
XX Excitation-secretory uncoupling peptide(s) for inhibiting
PT neuro-transmitter release used particularly for treating muscle
PT spasticity, and for delivering drugs specifically to neural cells
XX
XX PS Claim 1; Page 30; 61pp; English.
XX
XX This sequence corresponds to residues 170-206 of the human 25 kD
CC synaptosomal associated protein (SNAP-25), and is a inhibitory agent of
CC the invention. The agents of the invention inhibit secretion of
CC neurotransmitter from neuronal cells and is an excitation-secretory
CC uncoupling peptide (I) of at least 20 amino acids (aa) all of which
CC correspond substantially to any one of AAM30097-W30102, or more
CC generally any (I) that inhibits 50% of catecholamine secretion from
CC bovine chromaffin cells at a concentration of 10 microm, especially 0.25
CC microm, or less. (I) are used, as a replacement for clostridium toxin, to
CC inhibit release of neurotransmitters from synaptic vesicles, specifically
CC for reducing muscle spasticity. Also (I) may be labelled to allow in
CC vivo imaging of intracellular distribution of (I). Compounds for
CC delivering the drug to neural cells provide targeted drug delivery, e.g.,
CC of substance P to brain tumours for induction of apoptosis. Unlike the
CC neurotoxins, (I) are not toxic or immunogenic and are more readily
CC available. Their therapeutic effect lasts for several days or weeks, so
CC lower doses or less frequent treatments are required.
XX
XX Sequence 37 AA:
SQ
Query Match 100.0%; Score 83; DB 18; Length 37;
Best Local Similarity 100.0%; Pred. No. 2,7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 1 SNKTRIDEANQRATKML 17
Db |||||||
18 SNKTRIDEANQRATKML 34
RESULT 8
AAR86823
ID AAR86823 standard; Peptide: 70 AA.
XX
XX AAR86823;
AC
XX 15-AUG-1996 (first entry)
DT
XX SNAP-25 residues 137-206.
DE
XX
XX VAMP; vesicle-associated membrane protein; SNAP-25; syntaxin;
KW neurotransmitter; neurotoxin; botulinum; botulism; cleavage;
KW substrate; antibody; detection; assay.
XX
XX Synthetic.
OS
XX
XX WO9533850-A1.
PN
XX
XX 14-DEC-1995.
PD
XX
XX 02-JUN-1995; 95WO-GB01279.
PF
XX
XX 03-JUN-1994; 94GB-0011138.
PR
XX

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PA (CAMR-) CAMR CENT APPLIED MICROBIOLOGY & RES.  
 PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
 XX  
 PI Hallis B, James BAF, Quinn CP, Shone CC;  
 XX WPI: 1996-040249/04.  
 DR  
 XX Assay for botulinum or tetanus toxin - by combining test cpd. with  
 PT substrate which is cleaved by the toxin, and antibody specific for  
 PT the cleaved but not uncleaved substrate  
 XX  
 XX Example 4: Page 19; 48pp; English.  
 XX  
 CC The botulinum neurotoxins possess highly specific zinc-endopeptidase  
 CC activities within their light sub-units. Depending on the neurotoxin  
 CC type these act to cleave small proteins within the nerve cell which are  
 CC involved in neurotransmitter release. Antibodies are used in assays  
 CC which detect cleaved but not uncleaved substrate. Assays for botulinum  
 CC types A and E use the present sequence as a substrate. The sequence is  
 CC SNAP-25 protein, residues 137-206.  
 XX  
 SQ Sequence 70 AA:  
 Query Match 100.0%; Score 83; DB 17; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 SNKTRIDEANORATKML 17  
 Db 51 SNKTRIDEANORATKML 67  
 RESULT 9  
 AAB15584  
 ID AAB15584 standard; peptide: 86 AA.  
 XX  
 AC AAB15584;  
 XX  
 DT 02-MAR-2001 (first entry)  
 XX  
 DE Human SNAP-25 N-terminal peptide #4.  
 XX  
 KW Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;  
 KW SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;  
 KW neurodegenerative disorder.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO200064932-A1.  
 XX  
 PD 02-NOV-2000.  
 XX  
 PF 18-FEB-2000; 2000WO-ES00058.  
 XX  
 PR 23-APR-1999; 99ES-0000844.  
 XX  
 XX (LIPO-) LIPOTEC SA.  
 PA  
 PI Blanes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;  
 PI Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;  
 PI Vinagre Bover S, Gutierrez Perez LM, Carbonell Castell T;  
 PI Perez Paya E;  
 XX  
 DR WPI: 2001-007091/01.  
 XX  
 PT New peptides containing amino acid sequences from known proteins for  
 PT treatment of neurological disorders -  
 XX  
 XX Claim 16; Page 32-33; 40pp; Spanish.  
 PS  
 CC The invention relates to new peptides comprising 3-30 contiguous amino  
 CC acids from the N-terminus of the protein SNAP-25  
 CC (synaptosomal-associated protein 25). The peptides AAB15581-B15586

CC represent examples of the peptides of the invention. The peptides have  
 CC neuronal exocytosis inhibitory activity and are used for treatment of  
 CC facial wrinkles and asymmetry and pathological neuronal  
 CC exocytosis-mediated pathological disorders and alterations manifested  
 CC e.g. by spasms and neurological and neurodegenerative disorders.  
 XX  
 SQ Sequence 86 AA:  
 Query Match 100.0%; Score 83; DB 22; Length 86;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 SNKTRIDEANORATKML 17  
 Db 67 SNKTRIDEANORATKML 83  
 RESULT 10  
 AAO15165  
 ID AAO15165 standard; peptide: 116 AA.  
 XX  
 AC AAO15165;  
 XX  
 DT 02-SEP-2002 (first entry)  
 XX  
 DE Clostridial neurotoxin protease substrate peptide 4.  
 XX  
 KW Clostridial neurotoxin substrate; botulinum neurotoxin substrate; FRET;  
 KW fluorescence resonant energy transfer assay; quenched-signal;  
 KW clostridial neurotoxin detection; food.  
 XX  
 OS Undefined.  
 OS  
 PN WO200225284-A2.  
 XX  
 PD 28-MAR-2002.  
 XX  
 PF 25-SEP-2001; 2001WO-US30188.  
 XX  
 PR 25-SEP-2000; 2000US-235050P.  
 XX  
 XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.  
 PA  
 PI Schmidt JI, Stafford RG;  
 PI WPI: 2002-499829/53.  
 XX  
 DR  
 XX  
 PT Substrate useful in e.g. an assay for the protease activity of  
 PT clostridial neurotoxin, comprises modified peptide or protein -  
 XX  
 XX Claim 22; Page 16; 48pp; English.  
 XX  
 CC The invention comprises clostridial neurotoxin substrate peptides which  
 CC can serve as fluorescence resonant energy transfer assay (FRET) or  
 CC quenched-signal substrates in assays for the proteolytic activities of  
 CC clostridial neurotoxins. The invention further comprises Clostridium  
 CC botulinum neurotoxin substrate peptides that can serve as immobilised  
 CC substrates (i.e. bound to a solid phase) in assays for the proteolytic  
 CC activities of clostridial neurotoxins. The clostridial (including the  
 CC Clostridium botulinum) neurotoxin substrate peptides are useful for  
 CC detecting the presence of clostridial neurotoxins in a sample (e.g. food  
 CC or an environmental sample). The present amino acid sequence represents a  
 CC clostridial neurotoxin substrate peptide of the invention.

XX Sequence 116 AA;  
SQ Query Match 100.0%; Score 83; DB 23; Length 116;  
Best Local Similarity 100.0%; Pred. No. 9.7e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKML 17  
Db 96 SNKTRIDEANORATKML 112  
|||||

RESULT 11  
AAW30103  
ID AAW30103 standard; peptide: 206 AA.  
XX AAW30103;  
AC AAW30103;  
XX 06-APR-1998 (first entry)  
XX  
XX Synaptosomal associated protein.  
XX  
XX Neurotransmitter secretion; inhibitor: neuronal cell; synaptic vesicle;  
KM excitation-secretory uncoupling peptide; catecholamine secretion;  
KM bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;  
KM synaptosomal associated protein; SNAP-25.  
XX  
XX Homo sapiens.  
OS  
XX MO9734620-A1.  
PN  
XX 25-SEP-1997.  
PD  
XX 18-MAR-1997; 97WO-US04393.  
PF  
XX 18-MAR-1996; 96US-0013599.  
PR  
XX (REGC ) UNIV CALIFORNIA.  
PA  
XX Montal M;  
PI  
XX WPI; 1997-479986/44.  
DR  
XX  
XX Excitation-secretory uncoupling peptide(s) for inhibiting  
PT neuro:transmitter release - used particularly for treating muscle  
PT spasticity, and for delivering drugs specifically to neural cells  
XX  
XX  
PS Disclosure; Page 27-28; 61pp; English.

XX This sequence represents the human 25 kD synaptosomal associated protein  
CC (SNAP-25), which is an inhibitory agent of the invention. The agents of  
CC the invention inhibit secretion of neurotransmitter from neuronal cells  
CC and is an excitation-secretory uncoupling peptide (1) of at least 20  
CC amino acids (aa) all of which correspond substantially to any one of  
CC AAW30097-W30102, or more generally any (1) that inhibits 50% of  
CC catecholamine secretion from bovine chromaffin cells at a concentration  
CC of 10 microm, especially 0.25 microm, or less. (1) are used, as a  
CC replacement for Clostridium toxin, to inhibit release of  
CC neurotransmitters from synaptic vesicles, specifically for reducing  
CC muscle spasticity. Also (1) may be labeled to allow in vivo imaging of  
CC intracellular distribution of (1). Compounds for delivering the drug to  
CC neural cells provide targeted drug delivery, e.g. of substance P to  
CC brain tumours for induction of apoptosis. Unlike the neurotoxins, (1) are  
CC not toxic or immunogenic and are more readily available. Their  
CC therapeutic effect lasts for several days or weeks, so lower doses or  
CC less frequent treatments are required.  
XX  
XX Sequence 206 AA;

Query Match 100.0%; Score 83; DB 18; Length 206;  
Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKML 17  
Db 187 SNKTRIDEANORATKML 203  
|||||

RESULT 12  
AAW79198  
ID AAW79198 standard; Protein: 206 AA.  
XX AAW79198;  
AC AAW79198;  
XX 25-NOV-1998 (first entry)  
XX  
XX Mouse SNAP-25 polypeptide.  
DE  
XX Hrs-2 polypeptide; ATP-prefering nucleotidase; SNAP-25; vesicle docking;  
KM calcium-regulated secretion; secretory vesicle; secretory process; brain;  
KM neurotransmitter release; presynaptic membrane; CNS disorder; depression;  
KM Parkinson's disease; endocrine system; hormonal imbalance; cell division;  
KM thought disorder; schizophrenia; degenerative disorder; anaesthesia; rat;  
KM immune system; antigen processing; immunomodulator; viral processing;  
KM central nervous system; vesicular release; affective disorder; human;  
KM anti-tumour application; membrane trafficking regulation; mouse.  
XX  
XX Mus sp.  
OS  
XX MO9838210-A2.  
PN  
XX 03-SEP-1998.  
PD  
XX 26-FEB-1998; 98WO-US03789.  
PF  
XX 26-FEB-1997; 97US-0039159.  
PR  
XX (STRD ) UNIV LELAND STANFORD JUNIOR.  
PA  
XX Bean AJ, Scheller RH;  
PI  
XX WPI; 1998-481140/41.  
DR  
XX N-PSDB; AAV57558.  
DR  
XX  
XX New isolated Hrs-2 nucleotidase - used in assays to identify  
PT compounds capable of modulating calcium-regulatory secretion of  
PT secretory vesicles, such as in neurotransmitter release  
XX  
XX  
PS Claim 16; Pages 42-44; 55pp; English.

XX This represents a mouse SNAP-25 polypeptide, a component of the protein  
CC polypeptides thought to underlie vesicle docking and fusion. The  
CC invention provides rat and human Hrs-2 polypeptides which are ATP-  
CC preferring nucleotidase that associate with SNAP-25. For identifying a  
CC compound capable of modulating calcium-regulated secretion of secretory  
CC vesicles, a SNAP-25 polypeptide can be contacted with a Hrs-2  
CC polypeptide. In the presence and absence of a test compound. The effect  
CC of the test compound on the extent of binding between the SNAP-25 and  
CC Hrs-2 polypeptides are measured and a compound is identified as effective  
CC if its measured effect on the extent of binding is above a threshold  
CC level. The products can be used for identifying drugs capable of  
CC affecting secretory processes, such as neurotransmitter release at the  
CC active zones of presynaptic membranes. Such drugs can be used for  
CC treating disorders or conditions of the central nervous system by  
CC selectively enhancing or inhibiting vesicular release in specific areas  
CC of the brain, including affective disorders (e.g. depression), disorders  
CC of thought (e.g. schizophrenia) and degenerative disorders (Parkinson's  
CC disease), as well as applications such as anaesthesia. The drugs can  
CC also be used therapeutically in other systems such as the endocrine  
CC system for treatment of hormonal imbalances, the immune system for  
CC intervention in antigen processing, secreted immunomodulators, and viral  
CC processing, as well as anti-tumour applications, such as regulation of  
CC membrane trafficking during rapid cell division.  
XX  
XX Sequence 206 AA;

Query Match 100.0%; Score 83; DB 19; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKML 17  
 |||  
 DB 187 SNKTRIDEANORATKML 203

RESULT 13  
 AAM43426  
 ID AAM43426 standard; Protein; 206 AA.  
 XX  
 AC AAM43426;  
 XX  
 DT 27-APR-1998 (first entry)  
 XX  
 DE Mouse synaptosomal-associated protein-25.  
 XX  
 KM Binding domain; mouse; syntaxin; synaptosomal-associated protein; CNS;  
 KM neurotransmitter; presynaptic membrane; central nervous system; tumour;  
 KM neurodegenerative disease; hormonal disorder; immunological disorder.  
 XX  
 OS Mus sp.  
 XX  
 PN US5693476-A.  
 XX  
 PD 02-DEC-1997.  
 XX  
 PF 24-FEB-1995; 95US-0393985.  
 XX  
 PR 24-FEB-1995; 95US-0393985.  
 XX  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 XX  
 PI Scheller RH;  
 XX  
 DR WPI; 1998-031743/03.  
 XX  
 DR N-PSDB; AAV01554.  
 XX  
 PT Screening assay for modulators of syntaxin binding - using peptide  
 PT comprising binding site of syntaxin, for identifying drugs useful  
 PT for treating CNS disorders, neuro-degenerative diseases, etc  
 XX  
 PS Disclosure; Column 67-72; 57pp; English.  
 XX  
 CC This amino acid sequence represents the mouse synaptosomal-associated  
 CC protein of 25 kD (SNAP-25). The invention relates to a method for  
 CC identifying a compound capable of affecting the binding of a  
 CC syntaxin-binding protein (SBP), e.g. SNAP-25, alpha-SNAP, n-secl or VAMP,  
 CC to syntaxin. The method comprises measuring the effect of the test  
 CC compound on the extent of binding between the SBP and the SBP-binding  
 CC site on syntaxin. The method can be used for identifying drugs capable  
 CC of inhibiting or stimulating neurotransmitter release at the active zones  
 CC of presynaptic membranes, which may be useful for treating CNS disorders,  
 CC affective or psychotic disorders, neurodegenerative diseases, hormonal or  
 CC immunological disorders or tumours.  
 XX  
 SQ Sequence 206 AA;

Query Match 100.0%; Score 83; DB 19; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKML 17  
 |||  
 DB 187 SNKTRIDEANORATKML 203

RESULT 14  
 AAU00246  
 ID AAU00246 standard; Protein; 206 AA.  
 XX

AC AAU00246;  
 XX  
 DT 12-SEP-2001 (first entry)  
 XX  
 DE Synaptosomal-associated protein, SNAP25.  
 XX  
 DE SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;  
 KM toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;  
 KM synaptosomal-associated protein; mutagenic; PCR primer; mouse;  
 KM N-ethylmaleimide-sensitive fusion protein;  
 KM soluble NSF-attachment protein receptor.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Cleavage-site 180..181  
 FT /note="Peptide bond susceptible to cleavage by  
 FT clostridial neurotoxin"  
 FT Cleavage-site 197..198  
 FT /note="Peptide bonds susceptible to cleavage by  
 FT clostridial neurotoxin"  
 XX  
 PN WO200118038-A2.  
 XX  
 PD 15-MAR-2001.  
 XX  
 PF 18-AUG-2000; 2000WO-GB03196.  
 XX  
 PR 20-AUG-1999; 99US-0149993.  
 XX  
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
 XX  
 PI Dolly JO, O'Sullivan GA, Mohammed N, Foran PG;  
 XX  
 DR WPI; 2001-226739/23.  
 XX  
 PT Treating a patient suffering from poisoning or at risk of poisoning by  
 PT a clostridial toxin, e.g. botulism, comprises administering a  
 PT toxin-resistant or toxin-inhibitory SNARE -  
 XX  
 PS Disclosure; Fig 8; 131pp; English.  
 XX  
 CC The sequence represents the amino acid sequence of synaptosomal-  
 CC associated protein; SNAP25. The sequence was used to  
 CC create SNAP-25 double/single point mutants and C-terminal deletion  
 CC mutants used in a new method of treating a patient suffering from  
 CC poisoning or at risk of poisoning by a clostridial toxin, comprising  
 CC supplying a SNARE (soluble (N-ethylmaleimide-sensitive fusion protein)-  
 CC attachment protein receptor) to a cell of the patient, where the SNARE is  
 CC resistant to proteolysis by the toxin (toxin-resistant SNARE) and/or is  
 CC capable of inhibiting the toxin (toxin-inhibitory SNARE). The protein can  
 CC be used in a method of treating a patient in need of inhibition of SNARE-  
 CC dependent exocytosis from a cell capable of performing SNARE-dependent  
 CC exocytosis, comprising supplying a fragment, variant, fusion or derivative  
 CC of a SNARE or an inhibitory SNARE to the cell of the patient. The toxin  
 CC resistant or toxin inhibitory SNARE or a recombinant polynucleotide  
 CC encoding the SNARE is useful in the manufacture of a medicament for the  
 CC treatment of a patient suffering from poisoning or at risk of poisoning  
 CC by clostridial toxin, e.g. from botulism or tetanus. The fragment,  
 CC variant, fusion or derivative of a SNARE or of an inhibitory SNARE, or a  
 CC recombinant polynucleotide encoding either of these SNARE polypeptides  
 CC are useful in the manufacture of medicament for the treatment of a  
 CC patient in need of inhibition of SNARE-dependent exocytosis from a cell  
 CC capable of performing SNARE-dependent exocytosis. The method of treatment  
 CC is relatively fast, thus alleviating the symptoms when most severe and  
 CC taking the patient out of critical state.  
 XX  
 SQ Sequence 206 AA;

Query Match 100.0%; Score 83; DB 22; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANORATKML 17  
|  
187 SNKTRIDEANORATKML 203

## RESULT 15

AAU00252 standard; Protein; 206 AA.

AAU00252;

12-SEP-2001 (first entry)

SNARE homologue, synaptosomal-associated protein, hSNAP25a.

SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;  
toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;  
synaptosomal-associated protein; hSNAP25a; human;  
N-ethylmaleimide-sensitive fusion;  
soluble NSF-attachment protein receptor.

Homo sapiens.

WO200118038-A2.

15-MAR-2001.

18-AUG-2000; 2000WO-GB03196.

20-AUG-1999; 99US-0149993.

(IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

Dolly JO, O'Sullivan GA, Mohammed N, Foran PG;

WPI: 2001-226739/23.

N-PSDB: AAS00369.

Treating a patient suffering from poisoning or at risk of poisoning by  
a clostridial toxin, e.g. botulism, comprises administering a  
toxin-resistant or toxin-inhibitory SNARE -

Disclosure; Fig 8; 131pp; English.

The sequence represents the amino acid sequence of SNARE homologue,  
synaptosomal-associated membrane protein, hSNAP25a, used during analysis  
of SNAP-25. SNAP-25 mutants were used in a new method of treating a  
patient suffering from poisoning or at risk of poisoning by a clostridial  
toxin, comprising supplying a SNARE (soluble (N-ethylmaleimide-sensitive  
fusion protein)-attachment protein receptor) to a cell of the patient,  
where the SNARE is resistant to proteolysis by the toxin (toxin-resistant  
SNARE) and/or is capable of inhibiting the toxin (toxin-inhibitory  
SNARE). The protein can be used in a method of treating a patient in need  
of inhibition of SNARE-dependent exocytosis from a cell capable of  
performing SNARE-dependent exocytosis, comprises supplying a fragment,  
variant, fusion or derivative of a SNARE or an inhibitory SNARE to the  
cell of the patient. The toxin resistant or toxin inhibitory SNARE or a  
recombinant polynucleotide encoding the SNARE is useful in the  
manufacture of a medicament for the treatment of a patient suffering from  
poisoning or at risk of poisoning by clostridial toxin, e.g. from  
botulism or tetanus. The fragment, variant, fusion or derivative of a  
SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding  
either of these SNARE polypeptides are useful in the manufacture of  
medicament for the treatment of a patient in need of inhibition of SNARE-  
dependent exocytosis from a cell capable of performing SNARE-dependent  
exocytosis. The method of treatment is relatively fast, thus  
alleviating the symptoms when most severe and taking the patient out of  
critical state.

Sequence 206 AA;

Best Local Similarity 100.0%, Pred. No. 1.8e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SNKTRIDEANORATKML 17  
|  
Db 187 SNKTRIDEANORATKML 203

Search completed: September 16, 2003, 19:26:26  
Job time : 12.1429 secs

Query Match 100.0%; Score 83; DB 22; Length 206;

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 2003, 19:11:55 ; Search time 29.4286 Seconds

(without alignments)  
329.187 Million cell updates/sec

Title: US-09-942-098-2

Perfect score: 1048

Sequence: 1 MARDADMRNLEEMQRRADQ.....SNKTRIDEANQRATKMLGSG 206

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

127863

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

# SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query	Match Length	ID	Description
1	1048	100.0	206	1	SN25_HUMAN
2	974	92.9	204	1	SN2A_CARAU
3	933.5	89.1	203	1	SN2B_CARAU
4	837.5	79.9	210	1	SN25_TORMA
5	618.5	59.0	212	1	SN25_DROME
6	609.5	58.2	211	1	SN23_HUMAN
7	255	24.3	263	1	SN30_ARATH
8	239	22.8	277	1	YMO5_CABEL
9	230	21.9	300	1	SN29_ARATH
10	191.5	18.3	251	1	SEC9_YEAST
11	175	16.7	651	1	SN29_YEAST
12	166	15.8	256	1	SN29_HUMAN
13	156.5	14.9	54	1	SN25_RABIT
14	143.5	13.7	1935	1	MYH7_RAT
15	141	13.5	257	1	SN29_YEAST
16	139.5	13.3	397	1	YMP7_YEAST
17	137.5	13.1	1934	1	MYH7_HUMAN
18	137.5	13.1	1935	1	MYH7_HUMAN
19	137.5	13.1	1938	1	MYH6_RAT
20	136	13.0	1937	1	MYH8_HUMAN
21	134.5	12.8	1935	1	MYH7_HUMAN
22	133.5	12.7	1938	1	MYH6_MOUSE
23	133	12.6	1938	1	MYH4_RABIT
24	132.5	12.6	257	1	MYH8_RAT
25	132.5	12.6	1939	1	MYH6_MESAU
26	132	12.6	1939	1	MYH1_HUMAN
27	132	12.6	1941	1	MYH2_HUMAN
28	131.5	12.5	244	1	MYH7_PAPHA
29	131.5	12.5	1084	1	MYSS_RABIT
30	131.5	12.5	1940	1	MYH3_HUMAN
31	130.5	12.5	1940	1	MYH3_RAT
32	129.5	12.4	1939	1	MYH6_HUMAN
33	125	11.9	1938	1	MYH8_HUMAN

34	124	11.8	1939	1	MYH4_HUMAN	Q9Y623 homo sapien
35	123	11.7	1940	1	MYH3_CHICK	P02565 gallus gall
36	121.5	11.6	1938	1	MYSS_CHICK	P13558 gallus gall
37	119.5	11.4	1102	1	MYSC_CHICK	P29616 gallus gall
38	119	11.4	249	1	STXA_HUMAN	O60439 homo sapien
39	118	11.3	1360	1	CING_XENLA	O9Ptd7 xenopus lae
40	114	10.9	1005	1	RA50_MERVA	O58718 methanococc
41	114	10.9	1679	1	YIO9_YEAST	P40457 saccharomyc
42	112.5	10.7	242	1	TPM1_PODCA	P41114 podocoryne
43	112	10.7	1962	1	MYSA_DROME	P05661 drosophila
44	111.5	10.6	1972	1	MYHB_MOUSE	O08638 mus musculu
45	111	10.6	1278	1	DYNA_HUMAN	Q14203 homo sapien

## ALIGNMENTS

RESULT 1	SN25_HUMAN	STANDARD:	PRT:	206 AA.
ID	SN25_HUMAN			
AC	P13795: P36974:			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Synaposomal-associated protein 25 (SNAP-25) (Super protein) (SUP).			
GN	SNAP25 OR SNAP.			
OS	Homo sapiens (Human),			
OS	Macaca mulatta (Rhesus macaque),			
OS	Mus musculus (Mouse),			
OS	Rattus norvegicus (Rat), and			
OS	Gallus gallus (Chicken).			
OC	Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi;			
OC	Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.			
OX	NCBI_TaxID=9606, 9544, 10090, 10116, 9031;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).			
RC	SPECIES=Human: TISSUE=Brain;			
RX	MEDLINE=94156217; PubMed=8112622;			
RA	Bark I., Wilson M.C.;			
RT	"Human cDNA clones encoding two different isoforms of the nerve			
RL	terminal protein SNAP-25.";			
RL	Gene 139:291-292(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human: TISSUE=Brain;			
RX	MEDLINE=94333829; PubMed=8056350;			
RA	Zhao N., Hashida H., Takahashi N., Sakaki Y.;			
RT	"Cloning and sequence analysis of the human SNAP25 cDNA.";			
RL	Gene 145:313-314(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.			
RC	SPECIES=Human: TISSUE=Skeletal muscle;			
RX	MEDLINE=96332494; PubMed=8760387;			
RA	Jagadeish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L.,			
RA	Gough K.H., Grusovin J., Verkuylen A., Cosgrove L., Alafaci A.,			
RT	Frenkel M.J., Ward C.W.;			
RT	"Insulin-responsive tissues contain the core complex protein SNAP-25			
RT	(synaposomal-associated protein 25) A and B isoforms in addition to			
RT	synaptaxin 4 and synaptobrevins 1 and 2.";			
RL	Biochem. J. 317:945-954(1996).			
RL	[4]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human:			
RX	MEDLINE=21638749; PubMed=11780052;			
RA	Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.C.R.,			
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,			
RA	Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beate D.M.,			
RA	Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,			
RA	Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,			
RA	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,			
RA	Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,			
RA	Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,			
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,			



Query Match 100.0%; Score 1048; DB 1; Length 206;  
Best Local Similarity 100.0%; Pred. No. 2,7e-62;  
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEDADMRNLEEMORADOLADESLSTRMQLVVEESKDAGIRTLVIMDEGEOLERI 60  
DB 1 MAEDADMRNLEEMORADOLADESLSTRMQLVVEESKDAGIRTLVIMDEGEOLERI 60  
QY 61 EEGMDIINKDKMAEKRLTDLGFCGICVPCPKIKSSDAYKKAMGNODGVVASOPARY 120  
DB 61 EEGMDIINKDKMAEKRLTDLGFCGICVPCPKIKSSDAYKKAMGNODGVVASOPARY 120  
QY 121 VDREOMAIISGFIIRVTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180  
DB 121 VDREOMAIISGFIIRVTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180  
QY 181 IMEKADSNKTRIDEANORATKMLGSG 206  
DB 181 IMEKADSNKTRIDEANORATKMLGSG 206

## RESULT 2

SN2B\_CARAU STANDARD; PRT; 204 AA.

AC P36977;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Synaptoosomal-associated protein 25a (SNAP-25a).  
GN SNAP-A.  
OS Carassius auratus (Goldfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Carassius.  
OX NCBI\_TaxID=7957;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Retina;  
RX MEDLINE=94068448; PubMed=8248151;  
RA Rislinger C., Larhammar D.;  
RT "Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).  
CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE SYNAPTIC FUNCTION OF SPECIFIC NEURONAL SYSTEMS. ASSOCIATES WITH PROTEINS INVOLVED IN VESICLE DOCKING AND MEMBRANE FUSION.  
CC -1- SUBCELLULAR LOCATION: COMPLEXED WITH MACROMOLECULAR ELEMENTS OF THE NERVE TERMINAL.  
CC -1- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.  
CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.  
CC -----  
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: L22973; AAA16537.1; -  
DR PIR: I50480; I50480.  
DR InterPro: IPR000928; SNAP-25.  
DR InterPro: IPR000727; T-SNARE.  
DR Pfam: PF00835; SNAP-25; 1.  
DR SMART: SM00397; t-SNARE; 2.  
DR PROSITE: PS50192; T-SNARE; 2.  
KW Synaptoosome; Neurone; Repeat; Coiled coil; Multigene family.  
FT DOMAIN 19 81 T-SNARE COILED-COIL HOMOLOG 1.  
FT DOMAIN 138 200 T-SNARE COILED-COIL HOMOLOG 2.  
FT DOMAIN 85 92 CYS-RICH.  
SQ SEQUENCE 204 AA; 22843 MW; 458BBECFC09189 CRC64;

Query Match 92.9%; Score 974; DB 1; Length 204;  
Best Local Similarity 93.2%; Pred. No. 1,9e-57;  
Matches 192; Conservative 6; Mismatches 6; Indels 2; Gaps 1;

QY 1 MAEDADMRNLEEMORADOLADESLSTRMQLVVEESKDAGIRTLVIMDEGEOLERI 60  
DB 1 MAEDADMRNLEEMORADOLADESLSTRMQLVVEESKDAGIRTLVIMDEGEOLERI 60  
QY 61 EEGMDIINKDKMAEKRLTDLGFCGICVPCPKIKSSDAYKKAMGNODGVVASOPARY 120  
DB 61 EEGMDIINKDKMAEKRLTDLGFCGICVPCPKIKSSDAYKKAMGNODGVVASOPARY 118  
QY 121 VDREOMAIISGFIIRVTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 180  
DB 119 VDREOMAIISGFIIRVTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDR 178  
QY 181 IMEKADSNKTRIDEANORATKMLGSG 206  
DB 179 IMEKADSNKTRIDEANORATKMLGSG 204

## RESULT 3

SN2B\_CARAU STANDARD; PRT; 203 AA.

AC P36978;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Synaptoosomal-associated protein 25b (SNAP-25b).  
GN SNAP-B.  
OS Carassius auratus (Goldfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Carassius.  
OX NCBI\_TaxID=7957;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Retina;  
RX MEDLINE=94068448; PubMed=8248151;  
RA Rislinger C., Larhammar D.;  
RT "Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).  
CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE SYNAPTIC FUNCTION OF SPECIFIC NEURONAL SYSTEMS. ASSOCIATES WITH PROTEINS INVOLVED IN VESICLE DOCKING AND MEMBRANE FUSION.  
CC -1- SUBCELLULAR LOCATION: COMPLEXED WITH MACROMOLECULAR ELEMENTS OF THE NERVE TERMINAL.  
CC -1- TISSUE SPECIFICITY: NEURONS OF THE NEOCORTEX, HIPPOCAMPUS, PIRIFORM CORTEX, ANTERIOR THALAMIC NUCLEI, PONTINE NUCLEI, AND GRANULE CELLS OF THE CEREBELLUM.  
CC -1- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.  
CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.  
CC -----  
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CC -----  
CC EMBL: L22976; AAA16538.1; -  
DR PIR: I50481; I50481.  
DR InterPro: IPR000928; SNAP-25.  
DR InterPro: IPR000727; T-SNARE.  
DR Pfam: PF00835; SNAP-25; 1.  
DR SMART: SM00397; t-SNARE; 2.  
DR PROSITE: PS50192; T-SNARE; 2.  
KW Synaptoosome; Neurone; Repeat; Coiled coil; Multigene family.  
FT DOMAIN 19 81 T-SNARE COILED-COIL HOMOLOG 1.  
FT DOMAIN 137 199 T-SNARE COILED-COIL HOMOLOG 2.  
FT DOMAIN 85 92 CYS-RICH.

FT CAROHD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 Query Match 89.1%; Score 933.5; DB 1; Length 203;  
 Best Local Similarity 89.3%; Pred. No. 8.4e-55;  
 Matches 184; Conservative 7; Mismatches 12; Indels 3; Gaps 1;

QY 1 MAEDAMRELEEMORADOLADESLESTRRLQLVEESKADGIRTLVLMDEGEQLERIE 60  
 DB 1 MADEADMNELTMDQARADQGDSELESTRRLQLVEESKADGIRTLVLMDEGEQLERIE 60  
 QY 61 EEGMDQIKDKMEAEKNTLDGKFCGLCYCPCKNKSSDAYKKANGNOGVVASOPARV 120  
 DB 61 EEGMDQIKDKMEAEKNTLDGKFCGLCYCPCKNKLGSG--QSWGNNOGVVASOPARV 117  
 QY 121 VDREOMAISSGFIIRVTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQRQIDR 180  
 DB 118 VDREOMAISSGFIIRVTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQRQIDR 177  
 QY 181 IMEKAADSKTRIDEANORATKMLGSG 206  
 DB 178 IMDMADSKTRIDEANORATKMLGSG 203

RESULT 4  
 SN25\_TORMA STANDARD: PRT; 210 AA.  
 ID SN25\_TORMA  
 AC P36976;  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Synaptosomal-associated protein 25 (SNAP-25).  
 OS Torpedo marmorata (Marbled electric ray).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Batrachia; Chondrichthyes;  
 CC Elasmobranchii; Squalea; Hypnosqualea; Pristiogadidae; Batoidae;  
 CC Torpediniformes; Torpedinidae; Torpedidae;  
 CC NCBI\_Taxid=7788;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Electric lobe;  
 RX MEDLINE=94043281; PubMed=8226991;  
 RA Risting C., Blomqvist A.G., Lundell I., Lambertsson A.,  
 RA Nassel D., Pieribone V.A., Brodin L., Larhammar D.,  
 RT "Evolutionary conservation of synaptosome-associated protein 25 kDa  
 RT (SNAP-25) shown by Drosophila and Torpedo cDNA clones.";  
 RL J. Biol. Chem. 268:24408-24414(1993).  
 CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE SYNAPTIC FUNCTION OF  
 CC SPECIFIC NEURONAL SYSTEMS. ASSOCIATES WITH PROTEINS INVOLVED IN  
 CC VESICLE DOCKING AND MEMBRANE FUSION.  
 CC -1- SUBCELLULAR LOCATION: COMPLEXED WITH MACROMOLECULAR ELEMENTS OF  
 CC THE NERVE TERMINAL.  
 CC -1- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.  
 CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: L22020; AAA49284.1; -.  
 DR PIR: I50552; I50552;  
 DR InterPro: IPR000928; SNAP-25.  
 DR InterPro: IPR000727; T-SNARE.  
 DR Pfam: PF00835; SNAP-25; 1.  
 DR SMART: SM00397; t-SNARE; 2.  
 DR PROSITE: PS0192; T-SNARE; 2.  
 KW Synaptosome; Neurope; Repeat; Coiled coil.  
 FT DOMAIN 23 85 T-SNARE COILED-COIL HOMOLOGY 1.  
 FT DOMAIN 147 209 T-SNARE COILED-COIL HOMOLOGY 2.

FT DOMAIN 88 96 CYS-RICH.  
 SQ SEQUENCE 210 AA; 23652 MW; 58FE471A9234E8B1 CRC64;  
 Query Match 79.9%; Score 837.5; DB 1; Length 210;  
 Best Local Similarity 81.6%; Pred. No. 1.7e-48;  
 Matches 164; Conservative 16; Mismatches 18; Indels 3; Gaps 1;

QY 6 DMRELEEMORADOLADESLESTRRLQLVEESKADGIRTLVLMDEGEQLERIE 65  
 DB 10 DPRSEOMROCADITDESLESTRRLQLVEESKADGIRTLVLMDEGEQLERIE 69  
 QY 66 QINKDKMEAEKNTLDGKFCGLCYCPCKNKSSD--AYKKANGNOGVVASOPARV 122  
 DB 70 QINKDKMEAEKNTLDGKFCGLCYCPCKNKLFEGAGYKKVWGNNOGVVASOPARV 129  
 QY 123 FREOMAISSGFIIRVTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQRQIDR 182  
 DB 130 FREOMAISSGFIIRVTNDARENEMDENLEQVSGIIGNLRHMLDMGNEIDTQRQIDR 189  
 QY 183 EKADSKTRIDEANORATKML 203  
 DB 190 VKGDMKARIDEANORATKML 210

RESULT 5  
 SN25\_DROME STANDARD: PRT; 212 AA.  
 ID SN25\_DROME  
 AC P36975;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Synaptosomal-associated protein 25 (SNAP-25).  
 GN SNAP25.  
 OS Drosophila melanogaster (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydroidea; Drosophilidae; Drosophila.  
 CC NCBI\_Taxid=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Head;  
 RX MEDLINE=94043281; PubMed=8226991;  
 RA Risting C., Blomqvist A.G., Lundell I., Lambertsson A.,  
 RA Nassel D., Pieribone V.A., Brodin L., Larhammar D.,  
 RT "Evolutionary conservation of synaptosome-associated protein 25 kDa  
 RT (SNAP-25) shown by Drosophila and Torpedo cDNA clones.";  
 RL J. Biol. Chem. 268:24408-24414(1993).  
 CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE SYNAPTIC FUNCTION OF  
 CC SPECIFIC NEURONAL SYSTEMS. ASSOCIATES WITH PROTEINS INVOLVED IN  
 CC VESICLE DOCKING AND MEMBRANE FUSION.  
 CC -1- SUBCELLULAR LOCATION: COMPLEXED WITH MACROMOLECULAR ELEMENTS OF  
 CC THE NERVE TERMINAL.  
 CC -1- TISSUE SPECIFICITY: EXCLUSIVELY FOUND IN BRAIN AND GANGLIA.  
 CC -1- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.  
 CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: L22021; AAA16059.1; -.  
 DR EMBL: U01153; AAB39757.1; -.



DR EMBL; U81147; AAB39757.1; JOINED.  
 DR EMBL; U81148; AAB39757.1; JOINED.  
 DR EMBL; U81149; AAB39757.1; JOINED.  
 DR EMBL; U81150; AAB39757.1; JOINED.  
 DR EMBL; U81151; AAB39757.1; JOINED.  
 DR EMBL; U81152; AAB39757.1; JOINED.  
 DR FLYBase; FBgn0011288; Snp25.  
 DR GO; GO:0005486; C:Plasma membrane; NAS.  
 DR GO; GO:0005486; F:t-SNARE activity; NAS.  
 DR GO; GO:0007269; P:neurotransmitter secretion; NAS.  
 DR GO; GO:0016081; P:synaptic vesicle docking; NAS.  
 DR GO; GO:0016083; P:synaptic vesicle fusion; NAS.  
 DR InterPro; IPR000928; SNAP-25.  
 DR Pfam; PF00835; SNAP-25; 1.  
 DR SMART; SM00397; t-SNARE; 2.  
 DR PROSITE; PS50192; t-SNARE; 2.  
 KW Synaptosome; Neutrone; Repeat; Coiled coil.  
 FT DOMAIN 26 88 T-SNARE COILED-COIL HOMOLGY 1.  
 FT DOMAIN 148 210 T-SNARE COILED-COIL HOMOLGY 2.  
 FT DOMAIN 91 99 CYS-RICH.  
 SQ SEQUENCE 212 AA; 23685 MM; BCC90649A1AF3AC8 CRC64;

Query Match 59.0%; Score 618.5; DB 1; Length 212;  
 Best Local Similarity 62.9%; Pred. No. 3; 7e-34;  
 Matches 124; Conservative 29; Mismatches 43; Indels 1; Gaps 1;

OY 8 RNELEQRADQLADESLSTRMLDLVESKQAGRTVLMDEGEQLERIEGMDI 67  
 DB 15 KTELEELQINAGVADLESLSTRMLDLCESEKAGIRTVALLDDGEQLRIEIGMDI 74  
 OY 68 NKDKAEAKNLTDLGKFCGLVCPCNKLKSSDAYKKAQGNQDS-VVASOPARVVDREQ 126  
 DB 75 NADREAEKNTSGHEKCCGICVLPCKNSQSKREDGTWKGDGKVVNNQQRMDRRNG 134  
 OY 127 MAISGFIKRYTNDARENEDENLEQVSGIIGIRHMLDNGENIDFTQNRQIDRIMEKAD 186  
 DB 135 MMAQAGYIGITTDAREDEEMENGVNTMIGIRHMLDNGSELEQNQIRIDIRNKG 194  
 OY 187 SNKTRIDEANORATKML 203  
 DB 195 SNEARIIVANORAHQL 211

RESULT 6  
 SN23\_HUMAN STANDARD; PRT; 211 AA.  
 AC 000161; 000162; Q13602;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DE Synaptosomal-associated protein 23 (SNAP-23) (Vesicle-membrane fusion protein SNAP-23).  
 GN SNAP23.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-23A).  
 RC TISSUE=B-cell;  
 RX MEDLINE=96278745; PubMed=8663154;  
 RA Ravichandran V., Chawla A., Roche P.A.;  
 RT "Identification of a novel syntaxin- and synaptobrevin/VAMP-binding protein, SNAP-23, expressed in non-neuronal tissues.";  
 RL J. Biol. Chem. 271:13300-13303(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS SNAP-23A AND SNAP-23B).  
 RC MEDLINE=97224437; PubMed=9070898;  
 RA Mollinedo F., Lazo P.A.;  
 RT "Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23 in human neurophilis and HL-60 cells.";

RL Biochem. Biophys. Res. Commun. 231:808-812(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.  
 RA Nadal M., Area E., Mollinedo F., Estvill X., Lazo P.A.;  
 RT "Exon organization and chromosomal localization of human synaptosomal associated protein-23 (SNAP-23) gene and generation of isoforms by alternative splicing.";  
 RL Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-23A).  
 RC TISSUE=Cervix, Placenta, and Testis;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schermer A., Schein J.E., Jones S.J.M., Maira M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: ESSENTIAL COMPONENT OF THE HIGH AFFINITY RECEPTOR FOR THE GENERAL MEMBRANE FUSION MACHINERY AND AN IMPORTANT REGULATOR OF TRANSPORT VESICLE DOCKING AND FUSION.  
 CC -1- SUBUNIT: BINDS TIGHTLY TO MULTIPLE SYNTAXINS AND SYNAPTOBREVIN/VAMPs.  
 CC -1- SUBCELLULAR LOCATION: MAINLY LOCALIZED TO THE PLASMA MEMBRANE.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms-2;  
 CC Name=SNAP-23a;  
 CC IsoId=000161-1; Sequence=Displayed;  
 CC Name=SNAP-23b;  
 CC IsoId=000161-2; Sequence=VSP\_006187, VSP\_006188;  
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST LEVELS WHERE FOUND IN PLACENTA.  
 CC -1- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.  
 CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.  
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 CC -----  
 DR EMBL; U55936; AAC50537.1; -;  
 DR EMBL; Y09567; CAA70760.1; -;  
 DR EMBL; Y09568; CAA70761.1; -;  
 DR EMBL; AJ011915; CAA09864.1; -;  
 DR EMBL; BC000148; AAH00148.1; -;  
 DR EMBL; BC003686; AAH03686.1; -;  
 DR EMBL; BC022890; AAH22890.1; -;  
 DR PIR; JCS286; JCS296.  
 DR PIR; JCS287; JCS297.  
 DR Genew; HGNC:11131; SNAP23.  
 DR MIM; 602534; -;  
 DR GO; GO:0005886; C:plasma membrane; TAS.  
 DR GO; GO:0005803; C:secretory vesicle; TAS.  
 DR GO; GO:0005482; F:vesicle targeting; TAS.  
 DR GO; GO:0006944; P:membrane fusion; TAS.  
 DR GO; GO:0006903; P:non-selective vesicle targeting; TAS.

DR GO: 0006892; Post Golgi transport; TAS.  
 DR InterPro: IPR000928; SNAP-25.  
 DR InterPro: IPR000727; T-SNARE.  
 DR Pfam: PF00835; SNAP-25; 1.  
 DR SMART: SM00397; t-SNARE; 2.  
 DR PROSITE: PS50192; T-SNARE; 2.  
 KW Protein transport; Synaptosome; Coiled coil; Alternative splicing;  
 KW Membrane; Repeat.  
 FT DOMAIN 14 76 T-SNARE COILED-COIL HOMOLOG 1.  
 FT 208 T-SNARE COILED-COIL HOMOLOG 2.  
 FT VARSPIC 89 89 R -> S (in isoform SNAP-23b).  
 FT VARSPIC 90 142 /FTID-VSP\_006187.  
 FT VARSPIC 90 142 Missing (in isoform SNAP-23b).  
 FT FTID-VSP\_006187.  
 FT A -> V (in REF. 1).  
 SQ SEQUENCE 211 AA; 23354 MW; AC378E9786C3A239 CRC64;  
 Query Match 58.2%; Score 609.5; DB 1; Length 211;  
 Best Local Similarity 60.5%; Pred. No. 1,4e-33;  
 Matches 124; Conservative 29; Mismatches 41; Indels 11; Gaps 3;  
 QY 12 EEMORRADOADESLESTRMLQVLESKDAGIRTLVMDDEGEQLERIEEGMDQINKM 71  
 DB 7 EEIQQAHOITDESLESTRIRIIGLATESODAGIKITIMDEQEQNRLIEGIDQINKM 66  
 QY 72 KEAEKNTLDGKFCGLVCPCNKLK---SSDAYKKAMG---NNODGVVASOPARYVDER 124  
 DB 67 RETEKLTLELNKCCGLVCPCNRTKFEESGKAYKTTWGDGGENSPCNVYVSKGPCPTNGQ 126  
 QY 125 EQM---AISGGRFIRVTDARENEMDELEQVSGITGNLRHMLDMGNEIDTQNRQIDR 180  
 DB 127 IQDPTTGAASGGIKKITNDARENEMLEQVSGITGNLRHMLDMGNEIDTQNRQIDR 186  
 QY 181 IMEKADSNKTRIDEANORATKMLGS 205  
 DB 187 ITDKADTNDRIDIANARAKKLIDS 211  
 RESULT 7  
 SN30\_ARATH STANDARD; PRT; 263 AA.  
 AC 09LNG8:  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Putative SNAP25 homologous protein SNAP30 (AtSNAP30) (Synaptosomal-  
 associated protein SNAP25-like 3).  
 GN SNAP30 OR ATIG3890 OR P16A14.10.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=21016719; PubMed=11130712;  
 RA White O., Alonso J., Altrafi H., Araujo R., Bowman C.L., Brooks S.Y.,  
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Cressy T.H., Dewar K.,  
 RA Dunn P., Efgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,  
 RA Gull J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,  
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
 RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,  
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,  
 RA Miltischer J., Miranda M., Nguyen M., Niemman W.C., Osborne B.I.,  
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,  
 RA Uterback T., Van Aken S., Vayenberg M., Vysotskaia V.S., Walker M.,  
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.

RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
 thaliana.";  
 RL Nature 408:816-820(2000).  
 CC -1- FUNCTION: Vesicle trafficking protein that functions in the  
 CC secretory pathway (by similarity).  
 CC -1- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.  
 CC -1- SIMILARITY: Contains 1 t-SNARE coiled-coil homology domain.  
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 CC EMBL: AC068197; AAF79396.1; -.  
 DR PIR: A86272; A86272.  
 DR InterPro: IPR000727; T-SNARE.  
 DR SMART: SM00397; t-SNARE; 2.  
 DR PROSITE: PS50192; T-SNARE; 1.  
 KW Hypothetical protein; Transport; Protein transport; Membrane;  
 KW Coiled coil; Multigene family.  
 KW DOMAIN 198 260 T-SNARE COILED-COIL HOMOLOG.  
 SQ SEQUENCE 263 AA; 29075 MW; D55E680CEFE02C4 CRC64;  
 Query Match 24.3%; Score 255; DB 1; Length 263;  
 Best Local Similarity 29.1%; Pred. No. 3e-10;  
 Matches 62; Conservative 39; Mismatches 76; Indels 36; Gaps 3;  
 QY 12 EEMORRADOADESLESTRMLQVLESKDAGIRTLVMDDEGEQLERIEEGMDQINKM 71  
 DB 64 EELEKYAVYKAEBETGAVNNCLIKIADIRSDGARTLEMLHQEQEQRTHEMAVDMKDL 123  
 QY 72 KEAEKNTLDG-----KFCGLVCPCNKLKSDAKK-----AMGNND 110  
 DB 124 SRGEKLLNMGFSKPMKPKTKNTGTPIDPKSKSENEKEKIGCAGAKRSS 183  
 QY 111 GYVASOPARYVDEREGMAISGFIIRVTDARENEMDELEQVSGITGNLRHMLDMGNE 170  
 DB 184 GPALDPTNANLQKVEQ-----EKAKDDGLSDLSLTLGLKSAVAVMGSE 228  
 QY 171 IDTQNRQIDRIMEKADSNKTRIDEANORATKML 203  
 DB 229 IDKQNKALHLDGVDVDELNSRVGAGNARHLL 261  
 RESULT 8  
 YMO5\_CAEEL STANDARD; PRT; 277 AA.  
 AC P83351;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Hypothetical protein K02D10.5 on chromosome III.  
 GN K02D10.5.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,  
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,  
 RA Johnson L., Jones M., Kershaw J., Kirsten J., Laister N.,  
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Ritken L., Roopa A., Saunders D., Shonkhen R.,  
 RA Sims M., Shalton N., Smith A., Smith K., Sonhammer E., Staden R.,  
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,

RA Waterston R., Watson A., Weinstein L., Wilkinson-Sproat J.,  
RA Wohldman P.;  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans";  
RL Nature 368:32-38(1994).  
RN [2]  
RP REVISIONS.  
RA Waterston R.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.  
CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: L14710; AAK84538.1; -  
DR Morneped: K02D10.5; CE17152.  
DR InterPro: IPR000727; T-SNARE.  
DR SMART: SM00397; t-SNARE; 2.  
DR PROSITE: PS50192; T-SNARE; 2.  
KW Hypothetical protein; Protein transport; Synaptosome; Coiled coil;  
KW Repeat.  
FT DOMAIN 44 106 T-SNARE COILED-COIL HOMOLOG 1.  
FT DOMAIN 179 241 T-SNARE COILED-COIL HOMOLOG 2.  
SQ SEQUENCE 277 AA; 3115 MW; EF33EBA0ED2574B5 CRC64;  
Query Match 22.8%; Score 239; DB 1; Length 277;  
Best Local Similarity 28.0%; Pred. No. 3.5e-09;  
Matches 61; Conservative 43; Mismatches 88; Indels 26; Gaps 2;  
QY 9 NELEEMORRADQADELESTREMLQLVESKDGAGITLVMLDEGQLEIEEGMDQIN 68  
DB 34 DEADYVEREIEKTLQESLIDSTERSRHLNSENKIGTAAQLLEQRKLENTKNDLEIH 93  
QY 69 KDKAEAKNLTDGKFCGLCVCPCKNKSSDAYKKANGNNDGVVAOPARVVERGOMA 128  
DB 94 RTTOMTORNLSLKSFFG-----GMRKNFTKRPPEPTETPYQSKSASRSETATNL 147  
QY 129 ISGG-----FIRRYTNDARENEMDENTLEQVSGIIGLRLMALDMG 168  
DB 148 SSGGSGATFSGPGSGORTLTSSRSRAIKGTREAMEANDIDELDMNSANLRLQLGADLG 207  
QY 169 NEIDTONRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206  
DB 208 KEVDSONEMLDRIQYKAERNDIGIVRDODKQMKILGTG 245  
RESULT 9  
SN33-ARATH STANDARD; PRT; 300 AA.  
AC 0967P9;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE SNAP25 homologous protein SNAP33 (Synaptosomal-assocated  
DE protein SNAP25-like 1) (SNAP-25 like protein 1) (Snap25a).  
GN SNAP33 OR SNAP33B OR AT5G61210 OR MAF19.210 OR MAF19.2.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;  
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RC STRAIN=cv. Landsberg erecta, and cv. Columbia;  
RX MEDLINE=21490313; PubMed=11591731;  
RA Heese M., Gansel X., Sticher L., Wick P., Grebe M., Granier F.,  
RA Jurgens G.;

RT "Functional characterization of the KNO1LE-interacting t-SNARE  
RT ATSNAP33 and its role in plant cytokinesis";  
RL J. Cell Biol. 155:239-249(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=98069011; PubMed=9405937;  
RA Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,  
RA Tabata S.;  
RT "Structural analysis of Arabidopsis thaliana chromosome 5. II.  
RT Sequence features of the regions of 1,044,062 bp covered by thirteen  
RT physically assigned P1 clones.";  
RL DNA Res. 4:291-300(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;  
RT SSP Arabidopsis full length cDNA clones (RAFLs) sequenced by the  
RT SSP consortium (Salk/Stanford/PGEC).";  
RL submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
RA Feldmann K.;  
RT "Full-length cDNA from Arabidopsis thaliana.";  
RL submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RA Kim C.J., Chen H., Cheuk R.F., Shinn P., Bowser I., Carninci P.,  
RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,  
RA Hsuan V.W., Ishida J., Jones T., Kamita A., Karlin-Neumann G.,  
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,  
RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,  
RA Southwick A.M., Tang C.C., Toriumi M.J., Wallender E.K., Wong C.,  
RA Wu H.C., Yamada K., Yu G., Yuan S., Davis R.W., Theologis A.,  
RA Ecker J.R.;  
RT "Arabidopsis ORF clones";  
RL submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP CHARACTERIZATION, AND INTERACTION WITH KNO1LE AND STP121.  
RX MEDLINE=21576055; PubMed=11718726;  
RA Kargul J., Gansel X., Tyrrell M., Sticher L., Blatt M.R.;  
RT "Protein-binding partners of the tobacco syntaxin Ntsyrl.";  
RL FEBS Lett. 508:253-258(2001).  
RN [7]  
RP INDUCTION.  
RX PubMed=12746539;  
RA Wick P., Gansel X., Oulevey C., Page V., Studer I., Durst M.,  
RA Sticher L.;  
RT "The Expression of the t-SNARE ATSNAP33 Is Induced by Pathogens and  
RT Mechanical Stimulation";  
RL Plant Physiol. 132:343-351(2003).  
CC -1- FUNCTION: t-SNARE involved in diverse vesicle trafficking and  
CC membrane fusion processes, including cell plate formation. May  
CC function in the secretory pathway.  
CC -1- SUBUNIT: Interacts with the cytohesin-specific syntaxin KNO1LE  
CC and with STP121.  
CC -1- SUBCELLULAR LOCATION: Membrane-associated. Plasma membrane, some  
CC endomembrane compartment and cell plate in dividing cells.  
CC -1- TISSUE SPECIFICITY: Ubiquitous, with a strong expression in root  
CC tips, ovules, very young leaves, vascular tissue, hydathodes,  
CC stipules and the abscission and dehiscence zones of the siliques.  
CC -1- INDUCTION: Locally and systemically induced by pathogen infection  
CC and locally only by mechanical stresses.  
CC -1- MISCELLANEOUS: Specifically cleaved by the botulinum neurotoxins  
CC BotN/A and BotM/E.  
CC -1- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.  
CC -1- SIMILARITY: Contains 1 t-SNARE coiled-coil homology domain.  
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CC -----  
 DR EMBL: L34336; AAA35034.1; -  
 DR EMBL: 272794; CAA96992.1; -  
 DR PIR: A5100; A5100.  
 DR SCD: S0003241; SEC9.  
 DR InterPro: IPR000727; T\_SNARE.  
 DR SMART: SM00397; t-snare; 2.  
 DR PROSITE: PS50192; T\_SNARE; 2.  
 KW Protein transport; Repeat; Coiled coil.  
 FT DOMAIN 434 496 T-SNARE COILED-COIL. HOMOMOLOGY 1.  
 FT DOMAIN 588 650 T-SNARE COILED-COIL. HOMOMOLOGY 2.  
 SQ SEQUENCE 651 AA; 73623 MW; EA31AD73D20A10C7 CRC64;

Query Match 16.7%; Score 175; DB 1; Length 651;  
 Best Local Similarity 25.1%; Pred. No. 0.00013;  
 Matches 56; Conservative 37; Mismatches 86; Indels 44; Gaps 5;

OY 8 RNELEQMORRADOLADE-----SLESTRMLQLVESKDGIRITVIMLDEGEO 56  
 DB 412 KEERARQOQDEDAVDELKQIKFTKQSSVASTRTTLKMAQDAERAGNTLGMGHQSEQ 471  
 OY 57 LERIEGMDQJINKDKAEKMLTDLGKFCGLVC-----PCN-----KLKSSDAY 101  
 DB 472 LNVNEGNDLDMKQYKQVADKVAELKLNRSILAVHSNPNRSKRREEREQKLNRIE 531  
 OY 102 KKANGNODGVVASOPARV-----VDEREQ-----MAISGCFIRRTVNDARE 143  
 DB 532 EKLKREQTSQQLSOSTORIEGAMANNNNISEVEREYQKKNYLEKAKRYOFENDERDEME 591  
 OY 144 NEMDENLEQVSGIIGNLRHMLDMGNEIDTQNRQIDRIMEKAD 186  
 DB 592 LEIDRLDQIQOVSNRKLKMLTTGKEIDSOQKRLNNIESTD 634

RESULT 12  
 SN29\_HUMAN  
 ID SN29\_HUMAN STANDARD: PRT: 258 AA.  
 AC 095721.  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Synaptoosomal-associated-protein 29 (SNAP-29) (Vesicle-membrane fusion  
 DE protein SNAP-29) (Soluble 29 kDa NSF attachment protein).  
 GN SNAP29.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=99069409; PubMed=9852078;  
 RA Steegmaler M., Yang B., Yoo J.-S., Huang B., Shen M., Yu S., Luo Y.,  
 RA Scheller R.H.;  
 RT "Three novel proteins of the syntaxin/SNAP-25 family.";  
 RL J. Biol. Chem. 273:34171-34179(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Schardt A., Kraemer E.-M., Werner H., Nave K.-A.;  
 RT "Genomic organization of the human SNAP29 gene.";  
 RN Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinci P., Prange C.,  
 RA Raha S.S., Loguella N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosk S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -1- FUNCTION: INVOLVED IN MULTIPLE MEMBRANE TRAFFICKING STEPS.  
 CC -1- SUBUNIT: BINDS TIGHTLY TO MULTIPLE SYNTAXINS.  
 CC -1- SUBCELLULAR LOCATION: APPEARS TO BE MOSTLY MEMBRANE-BOUND,  
 CC PROBABLY VIA INTERACTION WITH SYNTAXINS, BUT A SIGNIFICANT PORTION  
 CC IS CYTOPLASMIC.  
 CC -1- TISSUE SPECIFICITY: FOUND IN BRAIN, HEART, KIDNEY, LIVER, LUNG,  
 CC PLACENTA, SKELETAL MUSCLE, SPLEEN AND PANCREAS.  
 CC -1- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.  
 CC -1- SIMILARITY: Contains 1 t-SNARE coiled-coil homology domain.

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CC -----  
 DR EMBL: AF15436; AAD11436.1; -  
 DR EMBL: AF278704; AAF91421.1; -  
 DR EMBL: BC009715; AAH09715.1; -  
 DR Genew: HGNC:11133; SNAP29.  
 DR MIM: 604202; -  
 DR GO: GO:0005886; C:Plasma membrane; TAS.  
 DR GO: GO:0005484; F:SNAP receptor activity; TAS.  
 DR GO: GO:0006887; P:exocytosis; TAS.  
 DR GO: GO:0006944; P:membrane fusion; TAS.  
 DR GO: GO:0006903; P:non-selective vesicle targeting; TAS.  
 DR InterPro: IPR000928; SNAP-25.  
 DR InterPro: IPR000727; T\_SNARE.  
 DR Pfam: PF00835; SNAP-25; 1.  
 DR SMART: SM00397; t-snare; 2.  
 DR PROSITE: PS50192; T\_SNARE; 1.  
 KW Protein transport; Synaptoosome; Coiled coil; Membrane.  
 FT DOMAIN 76 107 COILED COIL (POTENTIAL).  
 FT DOMAIN 196 258 T-SNARE COILED-COIL. HOMOMOLOGY.  
 SQ SEQUENCE 258 AA; 28970 MW; 7E1CDBA22D6F5A3C CRC64;

Query Match 15.8%; Score 166; DB 1; Length 258;  
 Best Local Similarity 26.1%; Pred. No. 0.0002;  
 Matches 60; Conservative 43; Mismatches 85; Indels 42; Gaps 7;

OY 5 ADMREL-EMQRRADOLADESLESTRMLQLVESKDGIRITVIMLDEGEOLERIEG 63  
 DB 39 ADROQYLRQEVLRRAEATA-----ASTSRSLAMESEKRVGAASSELARQGVLERTKM 94  
 OY 64 MDQIKDKAEKMLTDLGKFCGLVCPCNKLKSSDAYKKANGNODGVVASOPARVARE 123  
 DB 95 YDKMDQIKISOKHINSIKSVFGLV---NYFKSKPVETPP---EQNGTLLSOPNNRLKE 148  
 OY 124 -----REQMA-----ISGCFIRRTVND-----ARENEMDENLEQ 152  
 DB 149 AISTSKDEQAYQASHPLRLKLDPTDPPRGAGSAMSTDAYPKNPHLRAHQKIDSND 208  
 OY 153 VSGIIGNLRHMLDMGNEIDTQNRQIDRIMEKADSNKRTIDEANORATKM 202  
 DB 209 LSMGIGRLKDALGMQTEIEODDILRLTTRKVKVLDKVINIKSTERKRVOL 258

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RESULT 13
SN25_RABIT
ID SN25_RABIT STANDARD; PRT; 54 AA.
AC P55820;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25) (Super protein) (SUP)
DE (fragments).
GN SNAP25 OR SNAP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE AND CHARACTERIZATION.
RC STRAIN=New Zealand white; Tissue=Eye, and spinal cord;
RX MEDLINE=92044785; Pubmed=1941090;
RA Loewy A., Liu W.-S., Balingier C., Willard M.B.;
RT "The major 35S-methionine-labeled rapidly transported protein
RT (superprotein) is identical to SNAP-25, a protein of synaptic
RT terminals."
RT J. Neurosci. 11:3412-3421(1991).
CC -1- FUNCTION: INVOLVED IN THE MOLECULAR REGULATION OF NEUROTRANSMITTER
CC RELEASE. MAY PLAY AN IMPORTANT ROLE IN THE SYNAPTIC FUNCTION OF
CC SPECIFIC NEURONAL SYSTEMS. ASSOCIATES WITH PROTEINS INVOLVED IN
CC VESICLE DOCKING AND MEMBRANE FUSION (BT SIMILARITY).
CC -1- SUBCELLULAR LOCATION: COMPLEXED WITH MACROMOLECULAR ELEMENTS OF
CC THE NERVE TERMINAL.
CC -1- PTM: THE N-TERMINUS IS BLOCKED.
CC -1- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.
DR InterPro: IPR000928; SNAP-25.
DR Pfam: PF00835; SNAP-25; 1.
KW Neutrosc; Synaptosome.
FT NON_CONS 29 30
FT NON_CONS 45 46
FT NON_CONS 49 50
SQ SEQUENCE 54 AA; 6064 MW; 00014F740FEB29C5 CRC64;

Query Match 14.98; Score 156.5; DB 1; Length 54;
Best Local Similarity 41.0%; Pred. No. 0.00016;
Matches 43; Conservative 0; Mismatches 1; Indels 61; Gaps 2;

QY 32 MQLVVE-SKDAGRTVMDEGEOLERIEEGMDQINKMKREKNUITDLGRFGCLVC 90
DB 1 MQLVVESSSDAGRLXVLMDEGEOLE----- 28
QY 91 PCNKLKSSDAYKKRANGNNDGVVASOPARVYDEREQMAISGFTIR 135
DB 29 -----RYVDREQMAISGFTIR 45

RESULT 14
MYH7_RAT
ID MYH7_RAT STANDARD; PRT; 1935 AA.
AC P02564;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myosin heavy chain, cardiac muscle beta isoform (MyHC-beta).
GN MYH7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=90016823; Pubmed=2798112;
RA Kraft R., Bravo-Zehnder M., Taylor D., Leinwand L.A.;
RT "Complete nucleotide sequence of full length cDNA for rat beta
RT cardiac myosin heavy chain."

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RL Nucleic Acids Res. 17:7529-7530(1989).
RN [2]
RP DISCUSSION OF SEQUENCE.
RX MEDLINE=90133919; Pubmed=2614840;
RA McNally E.M., Kraft R., Bravo-Zehnder M., Taylor D., Leinwand L.A.;
RT "Full-length rat alpha and beta cardiac myosin heavy chain sequences.
RT Comparisons suggest a molecular basis for functional differences."
RL J. Mol. Biol. 210:665-671(1989).
RN [3]
RP SEQUENCE OF 1524-1935 FROM N.A.
RX MEDLINE=82220036; Pubmed=7045682;
RA Mahdavi V., Perlasamy M., Nadal-Ginard B.;
RT "Molecular characterization of two myosin heavy chain genes expressed
RT in the adult heart."
RL Nature 297:659-664(1982).
RN [4]
RP SEQUENCE OF 1871-1935 FROM N.A.
RC STRAIN=Wistar; Tissue=Heart;
RX MEDLINE=85179510; Pubmed=6241892;
RA Mahdavi V., Lompre A.M., Chambers A.P., Nadal-Ginard B.;
RT "Cardiac myosin heavy chain isozymic transitions during development
RT and under pathological conditions are regulated at the level of mRNA
RT availability."
RT Eur. Heart J. 5:181-191(1984).
CC -1- FUNCTION: MUSCLE CONTRACTION.
CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
CC -1- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
CC SUBFRAGMENT (S2).
CC -1- MISCELLANEOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' ATPASE
CC MYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE.
CC -1- SIMILARITY: Contains 1 myosin-like globular head domain.
CC -1- SIMILARITY: Contains 1 IQ domain.
CC -----
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CC -----
DR EMBL: X15939; CA34065.1; -
DR EMBL: J00752; AAA41654.1; -
DR EMBL: M32698; AAA41659.1; -
DR PIR: S06006; S06006.
DR HSSP: P08799; 1MND.
DR InterPro: IPR000048; IQ_region.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; Myosin_N.
DR InterPro: IPR002928; Myosin_tail.
DR Pfam: PF00612; IQ; 2.
DR Pfam: PF00663; myosin_head; 1.
DR Pfam: PF02736; Myosin_N; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR PRODOM: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR SMART: SM00242; MYSC; 1.
DR PROSITE: PS50096; IQ; 1.
DR MYOSIN: Muscle protein; Coiled coil; Thick filament; Actin-binding;
KW ATP-binding; Methylation; Alkylation; Multigene family;
KW Calmodulin-binding.
FT DOMAIN 1 780 MYOSIN HEAD-LIKE.

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FT DOMAIN 781 810 IQ.  
 FT DOMAIN 840 1935 COILED COIL (POTENTIAL).  
 FT NP\_BIND 178 185 ATP.  
 FT DOMAIN 655 677 ACTIN-BINDING.  
 FT DOMAIN 757 771 ACTIN-BINDING.  
 FT MOD\_RES 129 129 METHYLATION (TRI-) (POTENTIAL).  
 FT MOD\_RES 695 695 ALKYLATION (SH-1) (POTENTIAL).  
 FT MOD\_RES 705 705 ALKYLATION (SH-2) (POTENTIAL).  
 FT CONFLICT 1529 1531 IRK -> VRR (IN REF. 3).  
 FT CONFLICT 1731 1731 D -> H (IN REF. 3).  
 FT CONFLICT 1784 1784 N -> K (IN REF. 3).  
 FT CONFLICT 1851 1851 T -> N (IN REF. 3).  
 FT CONFLICT 1858 1858 R -> K (IN REF. 3).  
 SQ SEQUENCE 1935 AA; 223082 MW; C8376C324A7BD82B CRC64;

Query Match 13.7%; Score 143.5; DB 1; Length 1935;  
 Best Local Similarity 23.7%; Pred. No. 0.046;  
 Matches 56; Conservative 45; Mismatches 86; Indels 49; Gaps 9;

QY 7 MRNELPEMO-----RRADQLADESESTRMLQLVESKDGAGIRTLVMDGEQOLE-R 59  
 Db 1681 LQAELELRVAVQETESKRLAEDELIESERVOLHSQNTSLINQKKMDADLSQLOTE 1740  
 QY 60 IEEGMDQINKMKEAEKNTLDGKFCGLCYCPCKLKSSDAYKKAMGNODGVVASOPAR 119  
 Db 1741 VEEAVQECRAVEAEKAKAIYD---AAMMADELKKEQDTSALHERKMNMEQTIKDLQHR 1796  
 QY 120 VDEREQMAISG-----FIRRYTNDAREKEMDENLEQVSGIIGNLRHM-ALDMGN 169  
 Db 1797 -LDEAEQIALGKGKQLOKLEARYRELENEL-EAEORKNMESVGMKRSRRRIKELYQOT 1854  
 QY 170 EIDPTON-----ROIDRIMEKADSNKTR-----IDEANORA 199  
 Db 1855 EEDRKNTLRLODLVDLQILKVKAKYKQAEAEAEQADNTNLSKFRVQHELDAAEERA 1910

## RESULT 15

SN29\_RAT STANDARD; PRT: 257 AA.

AC 0922P6;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Synaposomal-associated protein 29 (SNAP-29) (Vesicle-membrane fusion protein SNAP-29) (Soluble 29 kDa NSF attachment protein) (GS32).  
 GN SNAP29.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_Taxid=10116;  
 RN [1]

RP SEQUENCE FROM N.A.  
 MEDLINE=99096689; Pubmed=9880331;  
 RA Wong S.H., Xu Y., Zhang T., Griffiths G., Lowe S.L., Subramaniam V.N.,  
 RA Seow K.T., Hong W.;  
 RT "GS32, a novel Golgi SNARE of 32 kDa, interacts preferentially with  
 RT syntaxin 6.";

RT Mol. Biol. Cell 10:119-134(1999).  
 CC -SUBUNIT: BINDS TIGHTLY TO MULTIPLE SYNTAXINS. PREFERENTIALLY BINDS  
 CC TO SYNTAXIN 6.  
 CC -TISSUE SPECIFICITY: Widely expressed.  
 CC -SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.  
 CC -SIMILARITY: Contains 1 t-SNARE coiled-coil homology domain.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; AF035822; AAC72291.1; -.

DR InterPro: IPR000928; SNAP-25.  
 DR InterPro: IPR000727; T-SNARE.  
 DR Pfam: PF00835; SNAP-25\_1.  
 DR SMART: SM00397; t-SNARE; 2.  
 DR PROSITE: PS50192; T-SNARE; 1.  
 KW Protein transport; Synaposome; Coiled coil.  
 FT DOMAIN 195 257 T-SNARE COILED-COIL HOMOMOLOGY.  
 SQ SEQUENCE 257 AA; 29070 MW; 9B9BC1A351CB1A3C CRC64;

Query Match 13.5%; Score 141; DB 1; Length 257;  
 Best Local Similarity 23.3%; Pred. No. 0.0085;  
 Matches 48; Conservative 42; Mismatches 78; Indels 38; Gaps 5;

QY 28 STRMLQLVESKDGAGIRTLVMDGEQOLEIRIEGMDQINKMKEAEKNTLDGKFCGL 87  
 Db 59 STSRSLFLMTESEKIGVASSSEELVRQGVLEHTEKMYDKMDQKMSQKHINISKVSFG 118  
 QY 88 CVCPCKLKSSDAYKKAMGNODGVVASOPARVV-----DEREQMAISGCFIRRYTN 139  
 Db 119 FI--NYFKSKPVPEPP---EQNGSIYVQPSRSRLKEAINTNSKQDESKYQASHPLRLRL-H 171  
 QY 140 DAR-----ENEDENLEQVSGIIGNLRHMLDMGNEIDPTQNR 176  
 Db 172 DAELDSVPASTVNTVEYYPKNSSLRAYHQKIDSNIDELSVGIRLKDIALGMQTEIERQDD 231  
 QY 177 QIDRIMEKADSNKTRIDEANORATKM 202  
 Db 232 ILDRITTKVDKLDVNIKSTKRYQL 257

Search completed: September 16, 2003, 19:27:06  
 Job time : 30.4286 secs

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## OM protein - protein search, using sw model

Run on: September 16, 2003, 19:11:55 ; Search time 1.14286 Seconds  
(Without alignments) 329.187 Million cell updates/sec

Title: US-09-942-098-1  
Perfect score: 39  
Sequence: 1 EAMQRATK 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	100.0	203	1 SN2B_CARAU	P36978 carassius a
2	39	100.0	204	1 SN2A_CARAU	P36977 carassius a
3	39	100.0	206	1 SN25_HUMAN	P13795 homo sapien
4	31	79.5	241	1 RRP_HRSV	P14156 human respi
5	31	79.5	241	1 RRP_HRSVA	P03421 human respi
6	31	79.5	241	1 RRP_HRSVL	P12579 human respi
7	31	79.5	244	1 1431_ECHGR	Q9u408 echinococcu
8	31	79.5	244	1 1431_ECHMU	Q24902 echinococcu
9	31	79.5	2337	1 TOR2_SCHPO	Q9y7k2 schistosach
10	30	76.9	175	1 ATPF_CHLVU	P56296 chlorella v
11	30	76.9	210	1 SN25_TORMA	P56976 torpedo mar
12	30	76.9	445	1 GUDH_ECOLI	P76637 escherichia
13	30	76.9	775	1 YTX1_XENLA	P14380 xenopus lae
14	30	76.9	953	1 SYV_VIBCH	Q9kfp3 vibrio chol
15	29	74.4	162	1 YLFF6_CAEEL	Q03558 caenorhabdi
16	29	74.4	340	1 NAS9_HORVU	Q9xfb7 hordeum vul
17	29	74.4	429	1 GUNC_FUSOX	P46237 fusarium ox
18	29	74.4	935	1 IF3B_MEDPR	Q9xhml mediago tr
19	28	71.8	149	1 RL9_XANAC	Q8pm12 xanthomonas
20	28	71.8	201	1 RS4_CORGL	Q8nsy4 corynebacte
21	28	71.8	241	1 RRP_HRSV1	P24567 human respi
22	28	71.8	274	1 TPML_METEN	Q25456 metapneus
23	28	71.8	302	1 EXRN_BPT3	P20321 bacterioph
24	28	71.8	489	1 SOFL_YEAST	P33750 saccharomyc
25	28	71.8	857	1 AMPN_STRLI	Q11010 streptomyce
26	28	71.8	1250	1 BXE_CLOBO	Q00456 clostridium
27	28	71.8	1250	1 BXE_CLOBU	P30995 clostridium
28	28	71.8	3866	1 HRX_MOUSE	P52005 mus musculu
29	28	71.8	3947	1 SID2_USTMA	Q43103 ustilago ma
30	27	69.2	83	1 MULT_PSEAF	P11221 pseudomonas
31	27	69.2	198	1 SPI6_YEAST	P17122 saccharomyc
32	27	69.2	241	1 RRP_BRSVA	P33454 bovine resp
33	27	69.2	241	1 RRP_ORSVW	P83956 ovine respi

34	27	69.2	267	1 PSB7_SCHPO	Q09841 schistosach
35	27	69.2	305	1 YBKB_ECOLI	P77367 escherichia
36	27	69.2	307	1 ODC2_YEAST	Q99297 saccharomyc
37	27	69.2	413	1 TGF2_XENLA	P17247 xenopus lae
38	27	69.2	439	1 NH97_CAEEL	Q9bjk5 caenorhabdi
39	27	69.2	473	1 GATB_MYCPU	Q98r09 mycoplasma
40	27	69.2	480	1 ORP2_HUMAN	Q9h1p3 homo sapien
41	27	69.2	532	1 SAT1_HUMAN	P43007 homo sapien
42	27	69.2	569	1 PGW2_YEAST	P37012 saccharomyc
43	27	69.2	675	1 YRRO_CAEEL	Q10000 caenorhabdi
44	27	69.2	679	1 VVRB_HAEIN	P45125 haemophilus
45	27	69.2	970	1 K852_HUMAN	Q9y6x9 homo sapien

## ALIGNMENTS

RESULT 1	ID	SN2B_CARAU	STANDARD:	PRT:	203 AA.
AC	P36978:	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)				
DT	15-SEP-2003 (Rel. 42, Last annotation update)				
DE	Synaposomal-associated protein 25B (SNAP-25B).				
GN	SNAP-B.				
OS	Carassius auratus (Goldfish).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;				
OC	Cyprinidae; Carassius.				
OX	NCBI_TaxID=7957;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Retina;				
RX	MEDLINE=94068448; PubMed=8248151;				
RA	Risinger C., Larhammar D.;				
RT	"Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.";				
RT	Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).				
RL	-1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE SYNAPTIC FUNCTION OF SPECIFIC NEURONAL SYSTEMS. ASSOCIATES WITH PROTEINS INVOLVED IN VESICLE DOCKING AND MEMBRANE FUSION.				
CC	-1- SUBCELLULAR LOCATION: COMPLEXED WITH MACROMOLECULAR ELEMENTS OF THE NERVE TERMINAL.				
CC	-1- TISSUE SPECIFICITY: NEURONS OF THE NEOCORTEX, HIPPOCAMPUS, PRIFORM CORTEX, ANTERIOR THALAMIC NUCLEI, PONTINE NUCLEI, AND GRANDULE CELLS OF THE CEREBELLUM.				
CC	-1- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.				
CC	-1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.				
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CC	EMBL: L22976; AAA16538.1; -.				
DR	PIR: I50481; I50481.				
DR	InterPro: IPR000928; SNAP-25.				
DR	InterPro: IPR000727; t-SNARE.				
DR	Pfam: PF00835; SNAP-25; 1.				
DR	SMART: SM00387; t-SNARE; 2.				
DR	PROSITE: PS50192; t-SNARE; 2.				
KW	Synaposome; Neutrone; Repeat;				
FT	DOMAIN 19				
FT	DOMAIN 137				
FT	DOMAIN 85				
FT	CYS-RICH.				
FT	CARBOHYD 77				
FT	CARBOHYD 185				
FT	SEQUENCE 203 AA; 22664 MW; BDFBDEBDJ7D6D7 CRG64;				

Query Match 100.0%; Score 39; DB 1; Length 203;  
 Best Local Similarity 100.0%; Pred. No. 0.14;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANORATK 8  
 |||||  
 Db 191 EANORATK 198

RESULT 2  
 SNA\_CARAU STANDARD; PRT; 204 AA.  
 ID SNA2\_CARAU  
 AC P36977;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Synaptoosomal-associated protein 25a (SNAP-25a).  
 GN SNAP-A.  
 OS Carassius auratus (Goldfish).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Carassius.  
 OX NCBI\_TaxID=7957;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Retina;  
 RX MEDLINE=94068448; PubMed=8248151;  
 RA Rislanger C., Larhammar D.;  
 RT "Multiple loci for synapse protein SNAP-25 in the tetraploid  
 RT goldfish.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).  
 CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE SYNAPTIC FUNCTION OF  
 CC SPECIFIC NEURONAL SYSTEMS. ASSOCIATES WITH PROTEINS INVOLVED IN  
 CC VESICLE DOCKING AND MEMBRANE FUSION.  
 CC -1- SUBCELLULAR LOCATION: COMPLEXED WITH MACROMOLECULAR ELEMENTS OF  
 CC THE NERVE TERMINAL.  
 CC -1- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 t-SNARE COILED-COIL HOMOLOGY DOMAINS.  
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 CC -----  
 CC EMBL: L22973; AAA16537.1; -  
 CC PIR: I50480;  
 CC DR InterPro: IPR000928; SNAP-25.  
 CC DR InterPro: IPR000727; t-SNARE.  
 CC DR Pfam: PF00835; SNAP-25; 1.  
 CC DR SMART: SM00397; t-SNARE; 2.  
 CC DR PROSITE: PS50192; t-SNARE; 2.  
 CC KW Synaptoosome; Neurone; Repeat; Coiled coil; Multigene family.  
 CC FT DOMAIN 19 81 t-SNARE COILED-COIL HOMOLOG 1.  
 CC FT 200 200 t-SNARE COILED-COIL HOMOLOG 2.  
 CC FT DOMAIN 85 92 CYS-RICH.  
 CC SQ SEQUENCE 204 AA; 22843 MW; 458BBEFCFC09189 CRC64;

Query Match 100.0%; Score 39; DB 1; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 0.14;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EANORATK 8  
 |||||  
 Db 192 EANORATK 199

RESULT 3  
 SNA25\_HUMAN STANDARD; PRT; 206 AA.  
 ID SNA25\_HUMAN  
 AC P13795; P36974;

DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Synaptoosomal-associated protein 25 (SNAP-25) (Super protein) (SNP).  
 GN SNAP25 OR SNAP.  
 OS Homo sapiens (Human).  
 OS Macaca mulatta (Rhesus macaque),  
 OS Mus musculus (Mouse),  
 OS Rattus norvegicus (Rat), and  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606, 9544, 10090, 10116, 9031;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).  
 RC SPECIES=Human; TISSUE=Brain;  
 RX MEDLINE=94156217; PubMed=8112622;  
 RA Bark I., Wilson M.C.;  
 RT "Human cDNA clones encoding two different isoforms of the nerve  
 RT terminal protein SNAP-25.";  
 RL Gene 139:291-292(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Human; TISSUE=Brain;  
 RX MEDLINE=94333829; PubMed=8056350;  
 RA Zhao N., Hashida H., Takahashi N., Sakaki Y.;  
 RT "Cloning and sequence analysis of the human SNAP25 cDNA.";  
 RL Gene 145:313-314(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.  
 RC SPECIES=Human; TISSUE=Skeletal muscle;  
 RX MEDLINE=96332494; PubMed=8760387;  
 RA Jagadeish M.N., Fernandez C.S., Hewlsh D.R., Macaulay S.L.,  
 RA Gough K.H., Griscov J., Verkuylen A., Cosgrove L., Alafaci A.,  
 RA Frenkel M.J., Ward C.W.;  
 RT "Insulin-responsive tissues contain the core complex protein SNAP-25  
 RT (synaptoosomal-associated protein 25) A and B isoforms in addition to  
 RT syntaxin 4 and synaptobrevins 1 and 2.";  
 RL Biochem. J. 317:945-954(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Human;  
 RX MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,  
 RA Bailey J., Bayliss K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Cordy N.R.,  
 RA Coulson A., Coville G.J., Deardman R., Dhami P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Leharvalsh M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConachle L.J., McIay K., Murray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaidin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilting L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Macaca mulatta; TISSUE=Hippocampus;

RA Jensen M.J., Smith L.A.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=mouse; STRAIN=BALB/c;  
 RX MEDLINE=90078337; PubMed=2592413;  
 RA Oyler G.A., Higgins G.A., Hart R.A., Battenberg E., Billingsley M.,  
 Bloom F.E., Wilson M.C.;  
 RT "The identification of a novel synaptosomal-associated protein,  
 RT SNAP-25, differentially expressed by neuronal subpopulations.";  
 RL J. Cell Biol. 109:3039-3052(1989).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=mouse; STRAIN=C57BL/6; TISSUE=EYE;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Cantincci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Scherach A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [8]  
 RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).  
 RC SPECIES=rat;  
 RA Katakia M.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=rat; TISSUE=Brain;  
 RA Cho A.R., You K.H.;  
 RT "Cloning of the SNAP-25 gene from a rat brain cDNA library.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [10]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=chicken; TISSUE=Retina;  
 RX MEDLINE=91126080; PubMed=1992470;  
 RA Catsicas S., Larhammar D., Blomqvist A., Sanna P.P., Milner R.J.,  
 RA Wilson M.C.;  
 RT "Expression of a conserved cell-type-specific protein in nerve  
 RT terminals coincides with synaptogenesis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:785-789(1991).  
 RN [11]  
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.  
 RC SPECIES=chicken;  
 RX MEDLINE=93389738; PubMed=8377193;  
 RA Bark I.C.;  
 RT "Structure of the chicken gene for SNAP-25 reveals duplicated exon  
 RT encoding distinct isoforms of the protein.";  
 RL J. Mol. Biol. 233:67-76(1993).  
 RN [12]  
 RP PALMITOYLATION.  
 RC SPECIES=rat;  
 RX MEDLINE=93100552; PubMed=1281490;  
 RA Hess D.T., Slater T.M., Wilson M.C., Skene J.H.P.;  
 RT "The 25 kDa synaptosomal-associated protein SNAP-25 is the major  
 RT methionine-rich polypeptide in rapid axonal transport and a major  
 RT substrate for palmitoylation in adult CNS.";  
 RL J. Neurosci. 12:4634-4641(1992).  
 RN [13]

RP SUBCELLULAR LOCATION OF RNA TRANSCRIPTS.  
 RC SPECIES=rat;  
 RX MEDLINE=96346613; PubMed=8738135;  
 RA Jacobsson G., Piehl F., Bark I.C., Zhang X., Meister B.;  
 RT "Differential subcellular localization of SNAP-25a and SNAP-25b RNA  
 RT transcripts in spinal motoneurons and plasticity in expression after  
 RT nerve injury.";  
 RL Brain Res. Mol. Brain Res. 37:49-62(1996).  
 CC -1- FUNCTION: tSNARE involved in the molecular regulation of the  
 CC neurotransmitter release. May play an important role in the  
 CC synaptic function of specific neuronal systems. Associates with  
 CC proteins involved in vesicle docking and membrane fusion.  
 CC -1- SUBUNIT: Binds to syntaxin-1.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Comment=isoforms differ by the usage of two alternative  
 CC homologous exons (3a and 3b) which encode for positions 56 to 94  
 CC and differ only in 9 positions out of 39;  
 CC Name=SNAP-25b;  
 CC IsoId=P13795-1; Sequence=Displayed;  
 CC Name=SNAP-25a;  
 CC IsoId=P13795-2; Sequence=VSP\_006186;  
 CC Note=has been shown to exist only in human and rat so far;  
 CC -1- TISSUE SPECIFICITY: NEURONS OF THE NEOCORTEX, HIPPOCAMPUS,  
 CC PIRIFORM CORTEX, ANTERIOR THALAMIC NUCLEI, PONTINE NUCLEI, AND  
 CC GRANULE CELLS OF THE CEREBELLUM.  
 CC -1- PTM: PALMITOYLATED.  
 CC -1- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.  
 CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.  
 CC -----  
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 CC -----  
 DR EMBL: L19761; AAC37546.1; -;  
 DR EMBL: L19760; AAC37545.1; -;  
 DR EMBL: D21267; BAA22370.1; -;  
 DR EMBL: AL023913; CAB42860.1; -;  
 DR EMBL: AL023913; CAC34534.1; -;  
 DR EMBL: AF240770; AAF64477.1; -;  
 DR EMBL: M22012; AAA61741.1; -;  
 DR EMBL: BC018249; AAT18249.1; -;  
 DR EMBL: M57957; AAA49072.1; -;  
 DR EMBL: AF245227; AAF81202.1; -;  
 DR EMBL: AB003991; BAA20151.1; -;  
 DR EMBL: AB003992; BAA20152.1; -;  
 DR EMBL: L09253; AAA49070.1; -;  
 DR EMBL: L09254; AAA49070.1; JOINED.  
 Query Match 100.0%; Score 39; DB 1; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 0.14;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EANDRATK 8  
 Db 194 EANDRATK 201  
 RESULT 4  
 RRP\_HRSV STANDARD: PRT: 241 AA.  
 AC P14156;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE RNA polymerase alpha subunit (EC 2.7.7.48) (Phosphoprotein P).  
 GN P.  
 OS Human respiratory syncytial virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

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CC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCB1_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85263554; PubMed=3839520;
RA Lambden P.R.;
RT "Nucleotide sequence of the respiratory syncytial virus
  phosphoprotein gene.";
RL J. Gen. Virol. 66:1607-1612(1985).
CC -1- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
  POLYMERASE. IT MAY FUNCTION IN TEMPLATE BINDING.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
  [RNA](N).
CC -----
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CC -----
DR EMBL: M29342; AAA47416.1;
DR InterPro: IPR003487; Pnuemo_phosprot.
DR Pfam: PF02478; Pnuemo_phosprot; 1.
KM Transferase; RNA-directed RNA polymerase; Nucleocapsid;
  Phosphorylation.
FT MOD_RES 116 116 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 117 117 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 119 119 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 143 143 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 156 156 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 161 161 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 241 AA; 27162 MW; 3EEC20A478E4D42C CRC64;

Query Match 79.5%; Score 31; DB 1; Length 241;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EANDRATK 8
DB 12 DANNRATK 19

RESULT 5
RRPP_HRSVA STANDARD: PRT; 241 AA.
AC P03421;
ID 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RNA polymerase alpha subunit (EC 2.7.7.48) (Phosphoprotein P).
GN P.
OS Human respiratory syncytial virus (strain A2).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
  Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCB1_TaxID=11259;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85033973; PubMed=6548527;
RA Satake M., Elango N., Venkatesan S.;
RT "Sequence analysis of the respiratory syncytial virus phosphoprotein
  gene.";
RL J. Virol. 52:991-994(1984).
CC -1- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
  POLYMERASE. IT MAY FUNCTION IN TEMPLATE BINDING.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
  [RNA](N).
CC -----
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CC -----
DR EMBL: M1486; AAB59853.1;
DR PIR: A04037; RRMZ
DR InterPro: IPR003487; Pnuemo_phosprot.
DR Pfam: PF02478; Pnuemo_phosprot; 1.
KM Transferase; RNA-directed RNA polymerase; Nucleocapsid;
  Phosphorylation.
FT MOD_RES 116 116 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 117 117 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 119 119 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 143 143 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 156 156 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 161 161 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 241 AA; 27148 MW; 21A9E45CA2DFD50C CRC64;

Query Match 79.5%; Score 31; DB 1; Length 241;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EANDRATK 8
DB 12 DANNRATK 19

RESULT 6
RRPP_HRSVL STANDARD: PRT; 241 AA.
AC P12579;
ID 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RNA polymerase alpha subunit (EC 2.7.7.48) (Phosphoprotein P).
GN P.
OS Human respiratory syncytial virus (subgroup A / strain long).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
  Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCB1_TaxID=11260;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88323192; PubMed=3414184;
RA Lopez J.A., Villanueva N., Melero J.A., Portela A.;
RT "Nucleotide sequence of the fusion and phosphoprotein genes of human
  respiratory syncytial (RS) virus long strain: evidence of subtype
  genetic heterogeneity.";
RL Virus Res. 10:249-262(1988).
RN [2]
RP PHOSPHORYLATION.
RX MEDLINE=91259076; PubMed=2045795;
RA Navarro J., Lopez-Otin C., Villanueva N.;
RT "Location of phosphorylated residues in human respiratory syncytial
  virus phosphoprotein.";
RL J. Gen. Virol. 72:1455-1459(1991).
CC -1- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
  POLYMERASE. IT MAY FUNCTION IN TEMPLATE BINDING.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
  [RNA](N).
CC -----
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CC -----
DR EMBL: M2644; AAA47415.1;
DR PIR: S07428; RRMZPP.
DR InterPro: IPR003487; Pnuemo_phosprot.
DR Pfam: PF02478; Pnuemo_phosprot; 1.
KM Transferase; RNA-directed RNA polymerase; Nucleocapsid;

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KW Phosphorylation.
FT MOD_RES 116 116 PHOSPHORYLATION.
FT MOD_RES 117 117 PHOSPHORYLATION.
FT MOD_RES 119 119 PHOSPHORYLATION.
FT MOD_RES 143 143 PHOSPHORYLATION.
FT MOD_RES 156 156 PHOSPHORYLATION.
FT MOD_RES 161 161 PHOSPHORYLATION.
SQ SEQUENCE 241 AA; 27147 MW; DCB2D3942973DD59 CRC64;

Query Match 79.5%; Score 31; DB 1; Length 241;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 EANOATK 8
Db 12 DANNRATK 19

RESULT 7
1431_ECHGR STANDARD; PRT: 244 AA.
AC Q9U408: 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 14-3-3 protein homolog 1.
OS Echinococcus granulosis.
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC Cyclophyllidae; Taeniidae; Echinococcus.
OX NCBI_TaxID=6210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CW1:
RX MEDLINE=21182697; PubMed=11289064;
RA Siles-Lucas M., Nunes C.P., Zaha A.;
RT "Comparative analysis of the 14-3-3 gene and its expression in
RT Echinococcus granulosis and Echinococcus multilocularis
RT metacystodes.";
RL Parasitology 122:281-287(2001).
CC -1- SIMILARITY: Belongs to the 14-3-3 family.
CC -----
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CC -----
DR EMBL: AF207904; AAC19966.1; -
DR HSSP: P29312; 1A37
DR InterPro: IPR000308; 14-3-3.
DR Pfam: PF00244; 14-3-3; 1.
DR PRINTS: PR00305; 1433ZETA.
DR PRODOM: PD000600; 14-3-3; 1.
DR SMART: SM00101; 14-3-3; 1.
DR PROSITE: PS00796; 1433_1; FALSE_NEG.
DR PROSITE: PS00797; 1433_2; 1.
KW Multigene family.
SQ SEQUENCE 244 AA; 27430 MW; 1FEC366D3054937B CRC64;

Query Match 79.5%; Score 31; DB 1; Length 244;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EANOATK 7
Db 155 EANOATK 161

RESULT 8
1431_ECHMU STANDARD; PRT: 244 AA.
ID 1431_ECHMU

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AC Q24902;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 14-3-3 protein homolog 1 (Emma14-3-3.1).
OS Echinococcus multilocularis.
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC Cyclophyllidae; Taeniidae; Echinococcus.
OX NCBI_TaxID=6211;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98226172; PubMed=9566521;
RA Siles-Lucas M., Felleisen R.S., Hemphill A., Wilson W., Gottstein B.;
RT "Stage-specific expression of the 14-3-3 gene in Echinococcus
RT multilocularis.";
RL Mol. Biochem. Parasitol. 91:281-293(1998).
CC -1- SIMILARITY: Belongs to the 14-3-3 family.
CC -----
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CC -----
DR EMBL: U63643; AAC48315.2; -
DR HSSP: P29312; 1A37.
DR InterPro: IPR000308; 14-3-3.
DR Pfam: PF00244; 14-3-3; 1.
DR PRINTS: PR00305; 1433ZETA.
DR PRODOM: PD000600; 14-3-3; 1.
DR SMART: SM00101; 14-3-3; 1.
DR PROSITE: PS00796; 1433_1; 1.
DR PROSITE: PS00797; 1433_2; 1.
KW Multigene family.
SQ SEQUENCE 244 AA; 27368 MW; 593881484ACFAC4C CRC64;

Query Match 79.5%; Score 31; DB 1; Length 244;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EANOATK 7
Db 155 EANOATK 161

RESULT 9
TOR2_SCHPO STANDARD; PRT: 2337 AA.
ID TOR2_SCHPO
AC Q9Y7K2; Q94507;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphatidylinositol 3-kinase tor2 (EC 2.7.1.137) (PI3-kinase)
DE (Ptdins-3-kinase) (PI3K).
CN TOR2 OR SPBC216.07C OR SPBC646.01C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Gobie A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

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RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volckert G., Aert R., Robben J., Grymptre B.,  
 RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moesli D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Medler H., Wandt R., Purnelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,  
 RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Kocher M., Gallardin C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,  
 RA Sipkavski G.V., Ussery D., Barrell B.G., Nuse P.,  
 RA "The genome sequence of Schizosaccharomyces pombe.",  
 RL Nature 415:871-880(2002).  
 RN [2]  
 RP IDENTIFICATION.  
 RX MEDLINE-21269225; PubMed-11096119;  
 RA Weisman R., Choder M.:  
 RT "The fission yeast TOR homolog, tor1+, is required for the response to  
 starvation and other stresses via a conserved serine.",  
 RL J. Biol. Chem. 276:7027-7032(2001).  
 CC -1- FUNCTION: Phosphatidylinositol 3-kinase homolog required for G1  
 CC progression (By similarity).  
 CC -1- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol = ADP +  
 CC 1-phosphatidyl-1D-myo-inositol 3-phosphate.  
 CC -1- SIMILARITY: BELONGS TO THE PI3/P14-KINASES FAMILY.  
 CC -1- SIMILARITY: Contains 15 HEAT repeats.  
 CC -----  
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 CC -----  
 DR EMBL: AL035216; CAN22805.1; -;  
 DR EMBL: AL049558; CAB40167.1; -;  
 DR PIR: T39913; T40577.  
 DR HSSP: P42345; LAUE.  
 DR GeneDB: Spombe; SPBC216.07c; -;  
 DR InterPro: IPR003151; FAT.  
 DR InterPro: IPR003152; FATC.  
 DR InterPro: IPR000357; HEAT\_repeat.  
 DR InterPro: IPR000403; PI3\_P14\_kinase.  
 DR Pfam: PF02260; FATC; 2.  
 DR Pfam: PF00454; PI3\_P14\_kinase; 2.  
 DR SMART: SM00146; PI3Kc; 1.  
 DR PROSITE: PSS0077; HEAT\_REPEAT; 1.  
 DR PROSITE: PSS00915; PI3\_4\_KINASE\_1; 1.  
 DR PROSITE: PSS0290; PI3\_4\_KINASE\_3; 1.  
 KW Transferrase; Kinase; Cell cycle; Repeat.  
 FT REPEAT 163 200 HEAT 1.  
 FT REPEAT 249 286 HEAT 2.  
 FT REPEAT 290 326 HEAT 3.  
 FT REPEAT 409 446 HEAT 4.  
 FT REPEAT 474 512 HEAT 5.  
 FT REPEAT 559 596 HEAT 6.  
 FT REPEAT 642 679 HEAT 7.  
 FT REPEAT 683 721 HEAT 8.  
 FT REPEAT 727 765 HEAT 9.  
 FT REPEAT 802 840 HEAT 10.  
 FT REPEAT 844 880 HEAT 11.  
 FT REPEAT 881 921 HEAT 12.  
 FT REPEAT 965 1004 HEAT 13.  
 FT REPEAT 1006 1043 HEAT 14.  
 FT REPEAT 1735 1772 HEAT 15.  
 FT DOMAIN 1990 2337 PI3K/P14K.

SQ SEQUENCE 2337 AA; 266376 MW; 190F448DA04FD2D9 CRC64;  
 Query Match 79.5%; Score 31; DB 1; Length 2337;  
 Best Local Similarity 75.0%; Pred. No. 1,1e+02;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EAMORATK 8  
 DB 1120 EASORSTK 1127  
 RESULT 10  
 ATPF\_CHLVU STANDARD; PRT; 175 AA.  
 ID ATPF\_CHLVU  
 AC P56296;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE ATP synthase B chain (EC 3.6.3.14) (Subunit I).  
 GN ATPF.  
 OS Chlorella vulgaris.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;  
 OC Chlorellaceae; Chlorella.  
 OX NCBI\_TaxID=3077;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IAM C-27 / Tamiya;  
 RX MEDLINE=97303241; PubMed=9159184;  
 RA Wakasugi T., Nagai T., Kapoor M., Sugita M., Ito M., Ito S.,  
 RA Tsudzuki J., Nakashima K., Tsudzuki T., Suzuki Y., Hamada A., Ohta T.,  
 RA Imanura A., Yoshinaga K., Sugitara M.;  
 RT "Complete nucleotide sequence of the chloroplast genome from the  
 RT green alga Chlorella vulgaris: the existence of genes possibly  
 RT involved in chloroplast division.",  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997).  
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate +  
 CC H(+) (out).  
 CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC  
 CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE  
 CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)  
 CC HAS THREE MAIN SUBUNITS: A, B AND C.  
 CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.  
 CC -1- SIMILARITY: BELONGS TO THE ATPASE B CHAIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AB001684; BAA57857.1; -;  
 DR PIR: T07210; T07210.  
 DR InterPro: IPR002146; ATPsynth\_B/B\_sub.  
 DR Pfam: PF00430; ATP-synt\_B; 1.  
 KW Hydrogen ion transport; Transmembrane; CF(0); Chloroplast.  
 FT TRANSMEM 19 38 POTENTIAL.  
 SQ SEQUENCE 175 AA; 19875 MW; 07F64D4B2C3BCF34 CRC64;  
 Query Match 76.9%; Score 30; DB 1; Length 175;  
 Best Local Similarity 75.0%; Pred. No. 12;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EAMORATK 8  
 DB 59 EADORATE 66  
 RESULT 11  
 SN25\_TORMA STANDARD; PRT; 210 AA.  
 ID SN25\_TORMA

AC P36976;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Synaptoosomal associated protein 25 (SNAP-25).  
 OS Torpedo marmorata (Marbled electric ray).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Squalia; Hypnosqualia; Pristigasterae; Batoidae;  
 OC Torpediniformes; Torpedinoidae; Torpedinidae; Torpedo.  
 OX NCBI\_Taxid=7788;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Electric lobe;  
 RX MEDLINE=9404381; PubMed=8226991;  
 RA Risinger C., Blomqvist A.G., Lundell I., Lambertsson A.,  
 RA Nasel D., Pierbone V.A., Brodin L., Larhammar D.,  
 RT "Evolutionary conservation of synaptoosome-associated protein 25 kDa  
 (SNAP-25) shown by Drosophila and Torpedo cDNA clones.";  
 RL J. Biol. Chem. 268:24408-24414(1993).  
 CC -I- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN THE SYNAPTIC FUNCTION OF  
 CC SPECIFIC NEURONAL SYSTEMS. ASSOCIATES WITH PROTEINS INVOLVED IN  
 CC VESICLE DOCKING AND MEMBRANE FUSION.  
 CC -I- SUBCELLULAR LOCATION: COMPLEXED WITH MACROMOLECULAR ELEMENTS OF  
 CC THE NERVE TERMINAL.  
 CC -I- SIMILARITY: BELONGS TO THE SNAP-25 FAMILY.  
 CC -I- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.  
 CC -----  
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 CC -----  
 CC EMBL: L22020; AAA49284.1; -  
 DR PIR: I50552; I50552.  
 DR InterPro: IPR000928; SNAP-25.  
 DR InterPro: IPR000727; T-SNARE.  
 DR Pfam: PF00835; SNAP-25.1.  
 DR SMART: SM00397; C-SNARE; 2.  
 DR PROSITE: PS50192; T-SNARE; 2.  
 DR Synaptoosome; Neurone; Repeat; Coiled coil.  
 KW DOMAIN 23 85 T-SNARE COILED-COIL HOMOMOLOGY 1.  
 FT DOMAIN 147 209 T-SNARE COILED-COIL HOMOMOLOGY 2.  
 FT DOMAIN 88 96 CYS-RICH.  
 SQ SEQUENCE 210 AA; 23652 MW; 58FE471A9234E8B1 CRC64;  
 Query Match 76.9%; Score 30; DB 1; Length 210;  
 Best Local Similarity 75.0%; Pred. No. 15;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EANKRATK 8  
 DB 201 EANKRATK 208  
 ID GUDH\_ECOLI STANDARD; PRT; 445 AA.  
 AC P76637; P78217; Q46914;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Glucarate dehydratase (EC 4.2.1.40) (GDH) (Glucd).  
 GN GUDP OR B2787 OR Z4102 OR ECS3647.  
 OS Escherichia coli, and  
 OS Escherichia coli 0157:H7.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_Taxid=562, 83334;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-O157:H7 / EDL933 / ATCC 700927;  
 RX MEDLINE=21074935; PubMed=11206551;  
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
 RA Grodebeck E.J., Davis N.W., Lim A., Dialanta E.T., Potamousis K.,  
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.;  
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";  
 RL Nature 409:529-533(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-O157:H7 / K1MD 0509952;  
 RX MEDLINE=21156231; PubMed=11258796;  
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Toke T.,  
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,  
 RA Kubara S., Shiba T., Hattori M., Shinagawa H.;  
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli  
 RT O157:H7 and genomic comparison with a laboratory strain K-12.";  
 RL DNA Res. 8:11-22(2001).  
 RN [4]  
 RP SEQUENCE OF 314-445 FROM N.A.  
 RC STRAIN-K12;  
 RX MEDLINE=97349980; PubMed=9205837;  
 RA Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,  
 RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,  
 RA Mizobuchi K., Mori H., Nakae S., Nakamura Y., Nashimoto H.,  
 RA Oshima T., Oyama S., Saito N., Sempel G., Satoh Y., Sivasubram S.,  
 RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,  
 RA Yamagata S., Horiiuchi T.;  
 RT "Construction of a contiguous 874-kb sequence of the Escherichia coli  
 RT K-12 genome corresponding to 50.0-68.8 min on the linkage map and  
 RT analysis of its sequence features.";  
 RL DNA Res. 4:91-113(1997).  
 RN [5]  
 RP SEQUENCE OF 1-14, AND CHARACTERIZATION.  
 RX MEDLINE=98447507; PubMed=9772162;  
 RA Hubbard B.K., Koch M., Palmer D.R., Babbitt P.C., Gerlt J.A.;  
 RT "Evolution of enzymatic activities in the enolase superfamily:  
 RT characterization of the (D)-glucarate/galactarate catabolic pathway  
 RT in Escherichia coli.";  
 RL Biochemistry 37:14369-14375(1998).  
 CC -I- FUNCTION: CATALYZES THE DEHYDRATION OF GLUCARATE TO 5-KETO-4-  
 CC DEOXY-D-GLUCARATE (5-KDGLDC). ALSO ACTS ON L-IDARATE.  
 CC -I- CATALYTIC ACTIVITY: D-glucarate - 5-dehydro-4-deoxy-D-glucarate +  
 CC H(2)O.  
 CC -I- PATHWAY: Glucarate catabolism: first step.  
 CC -I- SIMILARITY: BELONGS TO THE MANDELATE RACEMASE / MUCONATE  
 CC LACTONIZING ENZYME FAMILY. GUDC SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: U29581; AAA04037.1; -  
 DR EMBL: AE000362; AAC75829.1; -  
 DR EMBL: AE005507; AAG57900.1; -  
 DR EMBL: AF002562; BAB37070.1; -

DR EMBL: D90894; BAA15572.1; -.  
 DR PIR: G65060; G65060.  
 DR PIR: G91084; G91084.  
 DR PDB: 1EC7; 23-MAY-00.  
 DR PDB: 1EC8; 23-MAY-00.  
 DR PDB: 1EC9; 23-MAY-00.  
 DR PDB: 1EC9; 23-MAY-00.  
 DR PDB: 1JCT; 05-SEP-01.  
 DR PDB: 1JCT; 05-SEP-01.  
 DR EcoGene: Ecg13167; gudd.  
 DR InterPro: IPR001354; MR\_MLE.  
 DR Pfam: PF01188; MR\_MLE; 1.  
 DR Pfam: PF02746; MR\_MLE\_N; 1.  
 KM Lyase; Complete proteome; 3D-structure.  
 FT INIT\_MET 0  
 FT CONFLICT 309 312 PLAD -> RMRI (IN REF. 1; AAB40437).  
 SQ SEQUENCE 445 AA; 49010 MW; A46E1D91EBD446D6 CRC64;  
 Query Match 76.9%; Score 30; DB 1; Length 445;  
 Best Local Similarity 75.0%; Pred. No. 32;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EANORATK 8  
 DB 372 EGNORLTK 379  
 RESULT 13  
 YTX1\_XENLA STANDARD; PRT; 775 AA.  
 ID YTX1\_XENLA  
 AC P14380;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-APR-1990 (Rel. 14, Last annotation update)  
 DE Transposon Txi hypothetical 82 kDa protein (ORF 1).  
 OS Xenopus laevis (African clawed frog).  
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;  
 OC Xenopodidae; Xenopus.  
 OX NCBI\_TaxID=8335;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89384562; PubMed=2550791;  
 RA Garrett J.E., Knutzen D.S., Carroll D.;  
 RT "Composite transposable elements in the Xenopus laevis genome.";  
 RL Mol. Cell. Biol. 9:3018-3027(1989).  
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 CC EMBL: M26915; AAA49975.1; -.  
 DR PIR: A32494; A32494.  
 DR InterPro: IPR001878; znf\_CCHC.  
 DR Pfam: PF00098; zf\_CCHC; 1.  
 DR PRINTS: PR00939; C2HCZNFINGER.  
 DR SMART: SM00343; znf\_C2HC; 1.  
 KW Hypothetical protein; Transposable element.  
 SQ SEQUENCE 775 AA; 82335 MW; B8C361AEC65DD85B CRC64;

Query Match 76.9%; Score 30; DB 1; Length 775;  
 Best Local Similarity 75.0%; Pred. No. 57;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EANORATK 8  
 DB 594 EANHRSK 601

RESULT 14

SVY\_VIBCH STANDARD; PRT; 953 AA.  
 ID SVY\_VIBCH  
 AC O9KP73;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (VALRS).  
 GN VALS OR VC2503.  
 OS Vibrio cholerae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=666;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EI Tor N16961 / Serotype O1;  
 RX MEDLINE=20406833; PubMed=10952301;  
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,  
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,  
 RA Esmolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,  
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,  
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
 RA Fraser C.M.;  
 RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*  
 RT *cholerae*.";  
 RL Nature 406:477-483(2000).  
 CC -1- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate  
 CC + L-valyl-tRNA(Val).  
 CC -1- SUBUNIT: Monomer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.  
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 CC EMBL: AE004320; AAF5645.1; -.  
 DR PIR: E82068; E82068.  
 DR HSP: P96142; IGAX.  
 DR TIGR: VC2503;  
 DR InterPro: IPR002300; tRNA-synt\_1a.  
 DR InterPro: IPR001412; tRNA-synt\_1.  
 DR InterPro: IPR002303; tRNA-synt\_val.  
 DR Pfam: PF00133; tRNA-synt\_1; 1.  
 DR PRINTS: PR00986; tRNASYNTHVAL.  
 DR TIGRFAMs: TIGR00422; valS; 1.  
 DR PROSITE: PS00178; AA\_tRNA\_LIGASE\_1; 1.  
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;  
 KW Complete proteome.  
 FT SITE 42 52 "HIGH" REGION.  
 FT SITE 554 558 "KMSK" REGION.  
 FT BINDING 557 557 ATP (By SIMILARITY).  
 SQ SEQUENCE 953 AA; 108170 MW; D93471A33CF4F69C CRC64;

Query Match 76.9%; Score 30; DB 1; Length 953;  
 Best Local Similarity 75.0%; Pred. No. 71;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EANORATK 8  
 DB 730 EAOQRATR 737

RESULT 15  
 YLF6\_CAEEL STANDARD; PRT; 162 AA.  
 ID YLF6\_CAEEL  
 AC 003598;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)



DT 28-FEB-2003 (Rel. 41, last annotation update)  
DE Hypothetical protein C40H1.6 in chromosome III.  
GN C40H1.6.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
CC Rhabditidae; Pelodierinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPRAIN-Bristol NZ;  
RX MEDLINE=94150718; PubMed=7906398;  
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,  
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,  
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,  
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,  
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,  
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,  
RA Sims M., Smaildon N., Smith A., Smith M., Sonhammer E., Staden R.,  
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,  
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,  
RA Wohldman P.,  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans."  
RL Nature 368:32-38(1994).  
CC -1 SIMILARITY: STRONG, TO HUMAN CGI-126.  
CC -----  
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CC -----  
CC EMBL; Z19154; CAA79557.1; -.  
DR PIR; S28301; S28301.  
DR WormPep; C40H1.6; CE00114.  
KW Hypothetical protein.  
SQ SEQUENCE 162 AA; 18537 MW; 8DC03CE3BCE79D55 CRC64;

Query Match 74.4%; Score 29; DB 1; Length 162;  
Best Local Similarity 62.5%; Pred. No. 19;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 EANORATK 8  
1:1:1:1:1  
DB 56 ESNERGTK 63

Search completed: September 16, 2003, 19:27:05  
Job time : 2.14286 secs

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## OM protein - protein search, using sw model

Run on: September 16, 2003, 19:21:56 ; Search time 53.5065 Seconds  
(without alignments)  
370.249 Million cell updates/sec

Title: US-09-942-098-2

Perfect score: 1048  
Sequence: 1 MAEDADMRNLEEMQRRADQ.....SNKTRIDEANQRATKMLGSG 206

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

PIR\_76:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1048	100.0	206	A37861	synaptosomal-assoc
2	1048	100.0	206	A37823	nerve terminal pro
3	1048	100.0	206	A33623	synaptosomal-assoc
4	1004	95.8	206	I53735	nerve terminal pro
5	974	92.9	204	I50480	synapse protein SN
6	939	89.6	249	S38309	SNAP-25 protein SN
7	933.5	89.1	203	I50481	SNAP-25 protein SN
8	895	85.4	249	S38308	SNAP-25 protein -
9	837.5	79.9	210	I50552	synapse protein -
10	646	61.6	210	JC5512	SNARE protein 23 -
11	609.5	58.2	211	JC5296	vesicle-membrane f
12	541	51.6	234	T26553	hypothetical prote
13	512	48.9	158	JC5297	vesicle-membrane f
14	255	24.3	263	A86272	protein F16A14.10
15	239	22.8	786	S44837	KO2D10.1 protein -
16	191.5	18.3	251	T45613	SNAP25-like protei
17	186	17.7	56	S36812	probable synapse-a
18	175	16.7	651	A55100	SEC9 protein - yea
19	172.5	16.5	260	T16877	hypothetical prote
20	167	15.9	419	T40014	probable vesicular
21	152.5	14.6	46	S32362	SNAP receptor - bo
22	143.5	13.7	1935	S06006	myosin beta heavy
23	143	13.6	764	I51302	myosin heavy chain
24	142.5	13.6	1931	A59234	slow myosin heavy
25	139.5	13.3	397	S54018	DBP2 protein-inter
26	137.5	13.1	1934	T48153	myosin heavy chain
27	137.5	13.1	1935	A37102	myosin beta heavy
28	137.5	13.1	1938	S06005	myosin alpha heavy
29	136	13.0	1937	I38055	myosin heavy chain

30	134.5	12.8	1935	2	A59286	myosin heavy chain
31	133.5	12.7	1938	2	I49464	alpha cardiac myos
32	133	12.7	1938	2	A59293	skeletal myosin be
33	132.5	12.6	257	2	A02991	myosin heavy chain
34	132.5	12.6	557	2	A61236	myosin heavy chain
35	132.5	12.6	1939	2	I48175	myosin heavy chain
36	131.5	12.5	244	2	I36913	beta-myosin heavy
37	131.5	12.5	676	2	S00084	myosin heavy chain
38	131.5	12.5	1940	1	S04090	myosin heavy chain
39	131	12.5	876	2	A23767	myosin heavy chain
40	130.5	12.5	356	2	S15156	myosin heavy chain
41	130.5	12.5	385	2	C24263	myosin heavy chain
42	130.5	12.5	1940	1	A24922	myosin heavy chain
43	129.5	12.4	402	2	A37049	myosin alpha heavy
44	129.5	12.4	1939	1	A46762	myosin alpha heavy
45	123	11.7	936	2	S39083	myosin heavy chain

## ALIGNMENTS

## RESULT 1

A37861 synaptosomal-associated 25k protein - chicken

C:Species: Gallus gallus (chicken)

C:Date: 30-Apr-1991 #sequence\_revision 30-Apr-1991 #text\_change 21-Jul-2000

C:Accession: A37861

R:Castias, S.; Larhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C.  
Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991

A:Title: Expression of a conserved cell-type-specific protein in nerve terminals coln

A:Reference number: A37861; MUID:91126080; PMID:1992470

A:Accession: A37861

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-206 <CAT>

A:Cross-references: GB:M57957; NID:g212673; PIDN:AAA49072.1; PID:g212674

Query Match 100.0%; Score 1048; DB 2; Length 206;

Best local similarity 100.0%; Pred. No. 4; 6e-63;

Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAEDADMRNLEEMQRRADQ	LADESLSTRMLQLVRSKDG	AGIRTVLMDEQGEQLERI	60
DB	1	MAEDADMRNLEEMQRRADQ	LADESLSTRMLQLVRSKDG	AGIRTVLMDEQGEQLERI	60
QY	61	EEGMDQINKDKKEAKNLT	IGKFCGCLVCPCNKLKSD	AYKKAGNNDGVASQPARV	120
DB	61	EEGMDQINKDKKEAKNLT	IGKFCGCLVCPCNKLKSD	AYKKAGNNDGVASQPARV	120
QY	121	VDEREOMATISGFTIRVT	NDARENMDENLEOVSGII	GNLRHMLDNGNEITDTONR	180
DB	121	VDEREOMATISGFTIRVT	NDARENMDENLEOVSGII	GNLRHMLDNGNEITDTONR	180
QY	181	IMEKADSNKTRIDEANQR	ATKMLGSG 206		
DB	181	IMEKADSNKTRIDEANQR	ATKMLGSG 206		

## RESULT 2

167823 nerve terminal protein - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 05-Nov-1999

C:Accession: 167823

R:Bark, I.C.; Wilson, M.C.

Gene 139, 291-292, 1994

A:Title: Human cDNA clones encoding two different isoforms of the nerve terminal prot

A:Reference number: I53735; MUID:94156217; PMID:8112622

A:Accession: 167823

A>Status: preliminary; translated from GB/EHML/DBDU

A:Molecule type: mRNA

A:Residues: 1-206 <RES>

A:Cross-references: GB:LI9761; NID:g307427; PIDN:AAC37546.1; PID:g307428

C/Genetics:  
A/Gene: GDB:SNAP  
A/Cross-references: GDB:355671; OMIM:600322  
A/Map position: 20p11.2-20p11.2

Query Match	100.0%;	Score 1048;	DB 2;	Length 206;
Best Local Similarity	100.0%;	Pred. No. 4.6e-63;		
Matches 206;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	MAEDMDMNELEEMORRADQLADELESTRMLLOVEESKAGIRITVLMDEOSEOLERI	60
Db	1	MAEDMDMNELEEMORRADQLADELESTRMLLOVEESKAGIRITVLMDEOSEOLERI	60
Qy	61	EEGMDQINKDKKEAEKMLTDLGKFCGLCVCPCNKLKSSDAYKKAGNNQDGVASOPARV	120
Db	61	EEGMDQINKDKKEAEKMLTDLGKFCGLCVCPCNKLKSSDAYKKAGNNQDGVASOPARV	120
Qy	121	VDERQOMASGGFIRRYTNDARENEMDENLEQVSGITGNLPHMALDMGNEITDTONRQIDR	180
Db	121	VDERQOMASGGFIRRYTNDARENEMDENLEQVSGITGNLPHMALDMGNEITDTONRQIDR	180
Qy	181	IMEKADSNKTRIDEANORATKMLSG 206	
Db	181	IMEKADSNKTRIDEANORATKMLSG 206	

RESULT 3  
 A33623  
 synaptoosomal-associated 25K protein - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 04-Apr-1990 #sequence\_revision 04-Apr-1990 #text\_change 05-Nov-1999  
 C:Accession: A33623  
 R:Ovlier, G.A.; Higgins, G.A.; Hart, R.A.; Baltenberg, E.; Billingsley, M.; Bloom, F.E.;  
 J. Cell Biol. 109, 3039-3052, 1989  
 A:Title: The identification of a novel synaptoosomal-associated protein, SNAP-25, different  
 A:Reference number: A33623; MUID:90078337; PMID:2592413  
 A:Accession: A33623  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-206 <OYL>  
 A:Cross-references: GB:M22012; GB:X51673; NID:g200997; PIDN:AAA61741.1; PID:g200998

	Query Match	Similarity	100.0%	Score 1048:	DB 2:	length 206:
	Best Local	Similarity	100.0%	Pred. No. 4.6e-63:		
	Matches	206;	Conservative	0;	Mismatches	0;
					Indels	0;
					Gaps	0
QY	1	MAEDADMNRELEEMORRADQDLADESLESTRRMQLQVEESKDGAGRVLVLMDEGEQELERI	60			
Db	1	MAEDADMNRELEEMQRRADQDLADESLESTRRMQLQVEESKDGAGRVLVLMDEGEQELERI	60			
QY	61	EEGMOQINKDKMEAKRNLTDLCKFEGLCYCPENKLSAPYATKKAGNNODGYVASOPARY	120			
Db	61	EEGMOQINKDKMEAKRNLTDLCKFEGLCYCPENKLSAPYATKKAGNNODGYVASOPARY	120			
QY	121	VDEREQMAISGCFIRRTVNDARENEEMDEVLEFVSGITGLRHMALDMGNEITQNRQIDR	180			
Db	121	VDEREQMAISGCFIRRTVNDARENEEMDEVLEFVSGITGLRHMALDMGNEITQNRQIDR	180			
QY	181	IMEKADSNKTRIDEANQRAATKMLSGG	206			
Db	181	IMEKADSNKTRIDEANQRAATKMLSGG	206			

RESULT 4  
153735  
nerve terminal protein - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: 153735  
R:Bark, I.C.; Wilson, M.C.  
Gene 139, 291-292, 1994  
A:Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein  
A:Reference number: 153735; MUID:94156217; PMID:8112622

A:Accession: 153735  
A:Stratus: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-206 <RMS>  
A:Cross-references: GB:JL19760; NID:g307425; PIDN:AC37545.1; PID:g307426  
C:Genetics:  
A:Gene: GDB:SNAP  
A:Cross-references: GDB:355677; OMIM:600322  
A:Map position: 20p11.2-20p11.2

Query Match	95.8%	Score 1004;	DB 2;	Length 206;
Best Local Similarity	95.6%	Pred. No. 3.9e-60;		
Matches 197; Conservative	5;	Mismatches 4;	Indels 0;	Gaps 0;

[illegible]

RESULT 5  
150480  
synapse protein SNAP-25 - goldfish  
C:Species: Carassius auratus (goldfish)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C:Accession: 150480  
R:Risinger, C.; Larhammar, D.  
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993  
A:Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.  
A:Reference number: A49632; MIM:94068448; PMID:8248151  
A:Accession: 150480  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-204 <R15>  
A:Cross-references: GB:U22973; NID:g349426; PIDN:AA16537.1; PID:g349427  
C:Genetics:  
A:Gene: SNAP-25

Query Match	92.9%	Score 974	DB 2	Length 204
Best Local Similarity	93.2%	Pred. No. 3.8e-58		
Matches 192	Conservative	6	Mismatches 6	Indels 2
				Gaps 1
QY	1 MAEDADMRNELEEMORADOLADESLESTRRLMLQVEESKDGIFTLVLMDEQGOLERI	60		
Db	1 MAEDADMRNELESDMQQDLADESLESTRRLMLQVEESKDGIFTLVLMDEQGOLERI	60		
QY	61 EEGMQINKMDKEARKNLTDLCFEGCLCYCPCKNTKSSAPYKAKGANNODGVVASOPARY	120		
Db	61 EEGMQINKMDKADARKNLNDGCFEGCLSCPCPKNTKSGS--KAGANNODGVVASOPARY	118		
QY	121 VDEREQMASISGFIIRVTNDARENMEDNLEQVSGIIGLRLHMLDMGNEIDTQNRQIDR	180		
Db	119 VDEREQMASISGFIIRVTNDARENMEDNLEQVSGIIGLRLHMLDMGNEIDTQNRQIDR	178		
QY	181 IMEKADSKNTRIDEANQRTKMLGSG 206			
Db	179 IMEKADSKNTRIDEANQRTKMLGSG 204			

RESULT 6  
S38309  
SNAP-25 protein - chicken



```
QY      183 EKADSNKTRIDEANQATKML 203
          | | | | | | | | | |
Db      190 VKGDMNKARIDEANKHATKML 210
```

## RESULT 10

SNARE protein 23 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 05-Nov-1999  
C:Accession: J05512  
R:Araki, S.; Tamori, Y.; Kawanishi, M.; Shinoda, H.; Masugi, J.; Mori, H.; Niki, T.; Okabe, K. Biochem. Biophys. Res. Commun. 234, 257-262, 1997  
A:Title: Inhibition of the binding of SNAP-23 to syntaxin 4 by Munc18c.  
A:Reference number: J05512; MUID:97312558; PMID:9168999  
A:Accession: J05512  
A:Molecule type: mRNA  
A:Residues: 1-210 <ARA>  
A:Cross-references: DDBJ:AB000822; NID:g2189950; PIDN:BAA20345.1; PID:g1021177; PID:g2189950  
A:Comment: This protein is involved in the insulin-induced translocation of vesicles containing insulin.

Query Match	61.6%;	Score 646;	DB 2;	Length 210;
Best Local Similarity	62.3%;	Pred. No. 2.7e-36;		
Matches 127;	Conservative 32;	Mismatches 35;	Indels 10;	Gaps 3;

[illegible]

## RESULT 11

vesicle-membrane fusion protein SNAP-23A - human  
C:Species: Homo sapiens (man)  
C:Date: 02-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 05-Nov-1999  
C:Accession: J05296  
R:Mollinedo, F.; Lazo, P.A.  
Biochem. Biophys. Res. Commun. 231, 808-812, 1997  
A:Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-23  
A:Reference number: J05296; MUID:97224437; PMID:9070898  
A:Accession: J05296  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-211 <MOL>  
A:Cross-references: GB:J09567; NID:g1924941; PIDN:CA07060.1; PID:c290695; PID:g1924942  
A:Comment: This protein is involved in regulating exocytosis in human neutrophils, a certain

Query Match	58.2%;	Score 609.5;	DB 2;	Length 211;
Best Local Similarity	60.5%;	Pred. No. 7.4e-34;		
Matches 124;	Conservative 29;	Mismatches 41;	Indels 11;	Gaps 3;

[illegible]

Db	Qy	Db
12/	181	186
LOOPTGAASGGYIKRITNDAREDEMEENTLQVGSILGNLKDMLNIGNEIDAQNPQIKR	IMEKADSNKTRIDEANQRTKMLGS	
	I : : : : : I I I I I I : : : I	
	187	211
	ITDKADTNRRIDIANARAKKLIDS	

## RESULT 12

hypothetical protein Y22F5A.3 - *Caenorhabditis elegans*  
12033  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #extl\_change 15-Oct-1999  
C:Accession: Z26553  
R:Gardner, A.  
Submitted to the EMBL Data Library, January 1998  
A:Accession: Z26553  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-234 <WIL>  
A:Cross-references: EMBL:AL021479; PIDN:CAA16322.1; GSPDB:GN00023; CESP:Y22F5A.3  
A:Experimental source: clone Y22F5A  
C:Genetics:  
A:Gene: CESP:Y22F5A.3  
A:Map position: 5  
A:introns: 51/3; 82/1; 165/2; 213/3

Query Match	51.68	Score 541	DB 2	Length 234
Best Local Similarity	53.78	Pred. No. 3e-29		
Matches 108	Conservative 34	Mismatches 57	Indels 2	Gaps 1

QY	5	ADMRNELEEKORRAADQ	LADESLESTRRMALQ	LVESKDKAGIR	TLVMDLDEGQ	LETERIEGM	64	
		:    :	:    :	:    :	:    :	:    :		
Db	32	ADMSDELTGANG	IDEKTEIESLESTRRMAL	CESKEKEGIR	ITLVMDLDOGQ	ETREBEGAL	91	
QY	65	DOJNKMKEAKENL	DLGKEGCLGYCPO	NKLKSSP -	AYKKANGNDQ	GVAASQAPAVND	122	
		:    :    :	:    :	:    :	:    :	:    :		
Db	92	DTINQMKKEEDHL	KMEKCCGGLCYALPM	KTDIDFEKTEFA	KAMKKDDG	GVISQOPRITV	151	
QY	123	ERQOMASISG	FIRRVINDARENMEN	ENLVOYSGI	IGNLRH	HALDMGNEID	QONDIRIM	182
		:    :    :	:    :	:    :	:    :	:    :		
Db	152	GDSSMGPOGGY	ITIKINDAREDEME	NVQVSTYVGN	LARNALIM	DSLETVSNQ	NQNDRIH	211
QY	183	EKADSNKTRIDEA	NORATM	203				
		:    :    :	:    :	:    :	:    :	:    :		
Db	212	DKAQSNNEV	ESANKRAKMLI	232				

## RESULT 13

vesicle-membrane fusion protein SNAP-23B - human  
C:Species: Homo sapiens (man)  
C:Date: 02-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 05-Nov-1999  
C:Accession: J05297  
R:Mollinedo, F.; Lazo, P.A.  
Biochem. Biophys. Res. Commun. 231, 808-812, 1997  
A:Title: Identification of two isoforms of the vesicle-membrane fusion protein SNAP-2  
A:Reference number: J05296; MUID:97224437; PMID:9070898  
A:Accession: J05297  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-158 <MOL>  
A:Cross-references: GB:009568; NID:g1924943; PIDN:CAAF0761.1; PID:e290774; PID:g19249  
A:Experimental source: neutrophils  
A:Comment: This protein is involved in regulating exocytosis in human neutrophils, a

Query Match	48.9%	Score 512;	DB 2;	Length 158;
Best Local Similarity	53.6%	Pred. No. 1.7e-27;		
Matches 104; Conservative	22;	Mismatches 26;	Indels 42;	Gaps 1;

QY	12 EEMQRADQLADESLESTRMHLQVLESKDAGIRTLVMHDEQGEQLRIEESGMDQINKDM 711
D6	7 EEIQORAHQITDESLESTRRIIGLAIESODAGIKTITMLDEQKEOLNRIIEGLDQINKDM 666



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